SEQUENCE LISTING

<110> Smith, Hilda

<120> STREPTOCOCCUS SUIS VACCINES AND DIAGNOSTIC TESTS

<130> 2183-4726

<150> PCT/NL99/00460

<151> 1999-07-19

<150> EP98202465.5

<151> 1998-07-22

<150> EP98202467.1

<151> 1998-07-22

<160> 53

<170> PatentIn version 3.0

<210> 1

<211> 23

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 1

caaacgcaag gaattacggt atc 23

<210> 2

<211> 23

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 2

gagtatctaa agaatgccta ttg 23

<210> 3

<211> 20

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 3

ggcggtctag cagatgctcg 20

<210> 4

<211> 19

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 4

gcgaactgtt agcaatgac 19

<210> 5

<211> 21

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 5

ggctacatat aatggaagcc c 21

<210> 6

<211> 20

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 6

cggaagtatc tgggctactg 20

<210> 7

<211> 21

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 7

agctctaaca cgaaataagg c 21

<210> 8

<211> 21

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 8

gtcaaacacc ctggatagcc g 21

<210> 9

<211> 6992

<212> DNA

<213> Streptococcus suis

<220>

<221> misc_feature

<222> (1)..(6992)

<223> CPS 2

<400> 9

atcgccaaac gaaattggca ttatttgata tgatagcagt tgcaatttct gcaatcttaa 60

caagtcatat accaaatgct gatttaaatc gttctggaat ttttatcata atgatggttc 120

attattttgc atttttttata tctcgtatgc cagttgaatt tgagtataga ggtaatctga 180

tagagtttga aaaaacattt aactatagta taatatttgc aatttttctt acggcagtat 240

catttttgtt ggagaataat ttcgcacttt caagacgtgg tgccgtgtat ttcacattaa 300

taaacttcgt tttggtatac ctatttaacg taattattaa gcagtttaag gatagctttc 360

tattttcgac aatctatcaa aaaaagacga ttctaattac aacggctgaa cgatgggaaa 420

atatgcaagt tttatttgaa tcacataaac aaattcaaaa aaatcttgtt gcattggtag 480

ttttaggtac agaaatagat aaaattaatt tatcattacc gctctattat tctgtggaag 540

aagctataga gttttcaaca agggaagtgg tcgaccacgt ctttataaat ctaccaagtg 600

agtttttaga cgtaaagcaa ttcgtttcag attttgagtt gttaggtatt gatgtaagcg 660

ttgatattaa ttcattcggt tttactgcgt tgaaaaacaa aaaaatccaa ctgctaggtg 720

accatagcat tgtaactttt tccacaaatt tttataagcc tagtcatatc atgatgaaac 780

gacttttgga tatactcgga gcggtagtcg ggttaattat ttgtggtata gtttctattt 840

tgttagttcc aattattcgt agagatggtg gaccggctat ttttgctcag aaacgagttg 900

gacagaatgg acgcatattt acattctaca agtttcgatc gatgtatgtt gatgctgagg 960

agcgcaaaaa agacttgctc agccaaaacc agatgcaagg gtgggtatgt tttaaaatgg 1020

gaaaaacgat cctagaatta ctccaattgg acatttcata cgcaaaaaca agtttagacg 1080

agttaccaca gttttataat gttttaattg gcgatatgag tctagttggt acacgtccac 1140

ctacagttga tgaatttgaa aaatatactc ctggtcaaaa gagacgattg agttttaaac 1200

cagggattac aggtctctgg caggttagtg gtcgtagtaa tatcacagac ttcgacgacg 1260

tagttcggtt ggacttagca tacattgata attggactat ctggtcagat attaaaattt 1320

tattaaagac agtgaaagtt gtattgttga gagagggaag taagtaaaag tatatgaaag 1380

tttgtttggt cggttcttca gggggacatt tgactcactt gtatttgtta aaaccgtttt 1440

ggaaggaaga agaacgtttt tgggtaacat ttgataaaga ggatgcaaga agtcttttga 1500

agaatgaaaa aatgtatcca tgttactttc caacaaatcg caatctcatt aatttagtga 1560

aaaatacttt cttagctttc aaaattttac gtgatgagaa accagatgtt attatttcat 1620

ctggtgcggc cgttgctgtc cccttctttt acatcggaaa actatttgga gcaaagacga 1680

tttatattga agtatttgat cgagttaata aatctacatt aactggaaaa ctagtttatc 1740

ccgtaacaga tatttttatt gttcagtggg aagaaatgaa gaaggtatat cctaaatcta 1800

ttaacttggg gagtattttt taatgatttt tgtaacagta ggaactcatg aacaacagtt 1860

taatcgattg ataaaagaga ttgatttatt gaaaaaaaat ggaagtataa ccgacgaaat 1920

atttattcaa acaggatatt ctgactatat tccagaatat tgcaagtata aaaaatttct 1980

cagttacaaa gaaatggaac aatatattaa caaatcagaa gtagttattt gccacggagg 2040

ccccgctact tttatgaatt cattatccaa aggaaaaaaa caattattgt ttcctagaca 2100

aaaaaagtat ggtgaacatg taaatgatca tcaagtagag tttgtaagaa gaattttaca 2160

agataataat attttattta tagaaaatat agatgatttg tttgaaaaaa ttattgaagt 2220

ttctaagcaa actaacttta catcaaataa taatttttt tgtgaaagat taaaacaaat 2280

agttgaaaaa tttaatgagg atcaagaaaa tgaataataa aaaagatgca tatttgataa 2340

tggcttatca taatttttct cagattttac tggagaggga tacagatatt atcatcttct 2400

ctcaggagaa tgcacaccat tagttccttc agaatacctg tataattatt ttaaatattc 2460

tcaggattta tatgttgaat ttacaaaaga tgagcaaaaa tataaagaaa ataggatata 2520

tgaacgagtt aaatgttaca gattatttcc taatatatca gaaaaaacta ttgataatgt 2580

actgtttaga attttattaa gaatgtatcg agcttttgaa tactatttac aaagattgtt 2640

gtttattgat agaataaaaa acatggtcta agaataagat ttggttctaa ttgggtttcg 2700

cttccacatg attttgtggc aattctttta tcaaatgaaa acgaaacagc ttatttattt 2760

aagtaatcta aatgtccaga tgaactattt atacagacaa ttatagaaaa atatgaattt 2820

tcaaatagat tatctaaata tggaaattta agatatataa agtggaaaaa atcaacatct 2880

tctcctattg tctttacaga tgattctatt gatgaattgc taaatgcaag aaatttaggt 2940

tttttatttg ctagaaagtt aaaaatagaa aataaatcta aatttaaaga aattattact 3000

aaaaaataaa atagttgatt ttgtgagagt aatgtatgtt taaattattt aaatatgacc 3060

cggaatattt tatttttaag tacttctggt tgattatttt tattccagag caaaagtatg 3120

tatttttatt aatttttatg aatttaattt tatttcatat aaaatttttg aaaactaagc 3180

taatattaaa aaatgaaatt ttattgtttt tattatggtc tatattatgt tttgtttcag 3240

tagtcacaag tatgtttgtt gaaataaatt ttgaaagatt atttgcagat tttactgctc 3300

ccataatttg gattattgca ataatgtatt ataatttgta ttcatttata aatattgatt 3360

ataaaaaatt aaaaaatagt atctttttta gtttttagt tttattaggt atatctgcat 3420

tgtatattat tcaaaatggg aaagatattg tatttttaga cagacacctt ataggactag 3480

actatcttat aacaggcgtc aaaacaaggt tggttggctt tatgaactat cctacgttaa 3540

ataccactac aattatagtt tcaattccgt taatctttgc acttataaaa aataaaatgc 3600

aacaattttt tttcttgtgt cttgctttta taccgatcta tttaagtgga tcgagaattg 3660

gtagtttatc gctagcaata ttaattatat gcttgttatg gagatatata ggtggaaaat 3720

ttgcttggat aaaaaagcta atagtaatat ttgtaatact acttattatt ttaaatactg 3780

aattgcttta ccatgaaatt ttggctgttt ataattctag agaatcaagt aacgaagcta 3840

gatttattat ttatcaagga agtattgata aagtattaga aaacaatatt ttatttggat 3900

atggaatatc cgaatattca gttacgggaa cttggctcgg aagtcattca ggctatatat 3960

catttttta taaatcagga atagttgggt tgattttact gatgttttct ttttttatg 4020

ttataaaaaa aagttatgga gttaatgggg aaacagcact attttatttt acatcattag 4080

ccatattttt catatatgaa acaatagatc cgattattat tatattagta ctattctttt 4140

cttcaatagg tatttggaat aatataaatt ttaaaaagga tatggagaca aaaaatgaat 4200

gatttaattt cagttattgt accaatttat aatgtccaag attatcttga taaatgtatt 4260

aacagtatta ttaaccaaac atatactaat ttagaggtta ttctcgtaaa tgatggaagt 4320

actgatgatt ctgagaaaat ttgcttaaac tatatgaaga acgatggaag aattaaatat 4380

tacaagaaaa ttaatggcgg tctagcagat gctcgaaatt tcggactaga acatgcaaca 4440

ggtaaatata ttgcttttgt cgattctgat gactatatag aagttgcaat gttcgagaga 4500

atgcatgata atataactga gtataatgcc gatatagcag agatagattt ttgtttagta 4560

gacgaaaacg ggtatacaaa gaaaaaaaga aatagtaatt ttcatgtctt aacgagagaa 4620

gagactgtaa aagaattttt gtcaggatct aatatagaaa ataatgtttg gtgcaagctt 4680

tattcacgag atattataaa agatataaaa ttccaaatta ataatagaag tattggtgag 4740

gatttgcttt ttaatttgga ggtcttgaac aatgtaacac gtgtagtagt tgatactaga 4800

gaatattatt ataattatgt cattcgtaac agttcgctta ttaatcagaa attctctata 4860

aataatattg atttagtcac aagattggag aattacccct ttaagttaaa aagagagttt 4920

agtcattatt ttgatgcaaa agttattaaa gagaaggtta aatgtttaaa caaaatgtat 4980

tcaacagatt gtttggataa tgagttcttg ccaatattag agtcttatcg aaaagaaata 5040

cgtagatatc catttattaa agcgaaaaga tatttatcaa gaaagcattt agttacgttg 5100

tatttgatga aattttcgcc taaactatat gtaatgttat ataagaaatt tcaaaagcag 5160

tagaggtaaa aatggataaa attagtgtta ttgttccagt ttataatgta gataaatatt 5220

taagtagttg tatagaaagc attattaatc aaaattataa aaatatagaa atattattga 5280

tagatgatgg ctctgtagat gattctgcta aaatatgcaa ggaatatgca gaaaaagata 5340

aaagagtaaa aatttttttc actaatcata gtggagtatc aaatgctaga aatcatggaa 5400

taaagcggag tacagctgaa tatattatgt ttgttgactc tgatgatgtt gttgatagta 5460

gattagtaga aaaattatat tttaatatta taaaaagtag aagtgattta tctggttgtt 5520

tgtacgctac tttttcagaa aatataaata attttgaagt gaataatcca aatattgatt 5580

ttgaagcaat taataccgtg caggacatgg gagaaaaaaa ttttatgaat ttgtatataa 5640

ataatatttt ttctactcct gtttgtaaac tatataagaa aagatacata acagatcttt 5700

ttcaagagaa tcaatggtta ggagaagatt tacttttaa tctgcattat ttaaagaata 5760

tagatagagt tagttatttg actgaacatc tttatttta taggagaggt atactaagta 5820

cagtaaattc ttttaaagaa ggtgtgtttt tgcaattgga aaatttgcaa aaacaagtga 5880

tagtattgtt taagcaaata tatggtgagg attttgacgt atcaattgtt aaagatacta 5940

tacgttggca agtattttat tatagcttac taatgtttaa atacggaaaa cagtctattt 6000

ttgacaaatt tttaattttt agaaatcttt ataaaaaata ttattttaac ttgttaaaag 6060

tatctaacaa aaattctttg tctaaaaatt tttgtataag aattgtttcg aacaaagttt 6120

ttaaaaaaat attatggtta taataggaag atatcatgga tactattagt aaaatttcta 6180

taattgtacc tatatataat gtagaaaaat atttatctaa atgtatagat agcattgtaa 6240

atcagaccta caaacatata gagattcttc tggtgaatga cggtagtacg gataattcgg 6300

aagaaatttg tttagcatat gcgaagaaag atagtcgcat tcgttatttt aaaaaagaga 6360

acggcgggct atcagatgcc cgtaattatg gcataagtcg cgccaagggt gactacttag 6420

cttttataga ctcagatgat tttattcatt cggagttcat ccaacgttta cacgaagcaa 6480

ttgagagaga gaatgccctt gtggcagttg ctggttatga tagggtagat gcttcggggc 6540

atttcttaac agcagagccg cttcctacaa atcaggctgt tctgagcggc aggaatgttt 6600

gtaaaaagct gctagaggcg gatggtcatc gctttgtggt ggcctgtaat aaactctata 6660

aaaaagaact atttgaagat tttcgatttg aaaagggtaa gattcatgaa gatgaatact 6720

tcacttatcg cttgctctat gagttagaaa aagttgcaat agttaaggag tgcttgtact 6780

attatgttga ccgagaaaat agtatcacaa cttctagcat gactgaccat cgcttccatt 6840

gcctactgga atttcaaaat gaacgaatgg acttctatga aagtagagga gataaagagc 6900

tcttactaga gtgttatcgt tcatttttag cctttgctgt tttgttttta ggcaaatata 6960

atcattggtt gagcaaacag caaaagaagc tt 6992

<210> 10

<211> 239

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> ORF2Z

<400> 10

Ser Leu Asp Ile Asp His Met Met Glu Val Met Glu Ala Ser Lys Ser
1 5 10 15

Ala Ala Gly Ser Ala Cys Pro Ser Pro Gln Ala Tyr Gln Ala Ala Phe
20 25 30

Glu Gly Ala Glu Asn Ile Ile Val Val Thr Ile Thr Gly Gly Leu Ser
35 40 45

Gly Ser Phe Asn Ala Ala Arg Val Ala Arg Asp Met Tyr Ile Glu Glu
50 55 60

His Pro Asn Val Asn Ile His Leu Ile Asp Ser Leu Ser Ala Ser Gly
65 70 75 80

Glu Met Asp Leu Leu Val His Gln Ile Asn Arg Leu Ile Ser Ala Gly
85 90 95

Leu Asp Phe Pro Gln Val Val Glu Ala Ile Thr His Tyr Arg Glu His
100 105 110

Ser Lys Leu Leu Phe Val Leu Ala Lys Val Asp Asn Leu Val Lys Asn
115 120 125

Gly Arg Leu Ser Lys Leu Val Gly Thr Val Val Gly Leu Leu Asn Ile
130 135 140

Arg Met Val Gly Glu Ala Ser Ala Glu Gly Lys Leu Glu Leu Leu Gln
145 150 155 160

Lys Ala Arg Gly His Lys Lys Ser Val Thr Ala Ala Phe Glu Glu Met
165 170 175

Lys Lys Ala Gly Tyr Asp Gly Gly Arg Ile Val Met Ala His Arg Asn
180 185 190

Asn Ala Lys Phe Phe Gln Gln Phe Ser Glu Leu Val Lys Ala Ser Phe
195 200 205

Pro Thr Ala Val Ile Asp Glu Val Ala Thr Ser Gly Leu Cys Ser Phe
210 215 220

Tyr Ala Glu Glu Gly Gly Leu Leu Met Gly Tyr Glu Val Lys Ala
225 230 235

<210> 11

<211> 244

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> ORF2X

<400> 11

Met Lys Ile Ile Ile Pro Asn Ala Lys Glu Val Asn Thr Asn Leu Glu
1 5 10 15

Asn Ala Ser Phe Tyr Leu Leu Ser Asp Arg Ser Lys Pro Val Leu Asp
20 25 30

Ala Ile Ser Gln Phe Asp Val Lys Lys Met Ala Ala Phe Tyr Lys Leu
35 40 45

Asn Glu Ala Lys Ala Glu Leu Glu Ala Asp Arg Trp Tyr Arg Ile Arg
50 55 60

Thr Gly Gln Ala Lys Thr Tyr Pro Ala Trp Gln Leu Tyr Asp Gly Leu
65 70 75 80

Met Tyr Arg Tyr Met Asp Arg Arg Gly Ile Asp Ser Lys Glu Glu Asn
85 90 95

Tyr Leu Arg Asp His Val Arg Val Ala Thr Ala Leu Tyr Gly Leu Ile
100 105 110

His Pro Phe Glu Phe Ile Ser Pro His Arg Leu Asp Phe Gln Gly Ser
115 120 125

Leu Lys Ile Gly Asn Gln Ser Leu Lys Gln Tyr Trp Arg Pro Tyr Tyr
130 135 140

Asp Gln Glu Val Gly Asp Asp Glu Leu Ile Leu Ser Leu Ala Ser Ser
145 150 155 160

Glu Phe Glu Gln Val Phe Ser Pro Gln Ile Gln Lys Arg Leu Val Lys
165 170 175

Ile Leu Phe Met Glu Glu Lys Ala Gly Gln Leu Lys Val His Ser Thr
180 185 190

Ile Ser Lys Lys Gly Arg Gly Arg Leu Leu Ser Trp Leu Ala Lys Asn
195 200 205

Asn Ile Gln Glu Leu Ser Asp Ile Gln Asp Phe Lys Val Asp Gly Phe
210 215 220

Glu Tyr Cys Thr Ser Glu Ser Thr Ala Asn Gln Leu Thr Phe Ile Arg
225 230 235 240

Ser Ile Lys Met

<210> 12

<211> 481

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS2A

<400> 12

Met Lys Lys Arg Ser Gly Arg Ser Lys Ser Ser Lys Phe Lys Leu Val
1 5 10 15

Asn Phe Ala Leu Leu Gly Leu Tyr Ser Ile Thr Leu Cys Leu Phe Leu
20 25 30

Val Thr Met Tyr Arg Tyr Asn Ile Leu Asp Phe Arg Tyr Leu Asn Tyr
35 40 45

Ile Val Thr Leu Leu Leu Val Gly Val Ala Val Leu Ala Gly Leu Leu
50 55 60

Met Trp Arg Lys Lys Ala Arg Ile Phe Thr Ala Leu Leu Leu Val Phe
65 70 75 80

Ser Leu Val Ile Thr Ser Val Gly Ile Tyr Gly Met Gln Glu Val Val
85 90 95

Lys Phe Ser Thr Arg Leu Asn Ser Asn Ser Thr Phe Ser Glu Tyr Glu
100 105 110

Met Ser Ile Leu Val Pro Ala Asn Ser Asp Ile Thr Asp Val Arg Gln
115 120 125

Leu Thr Ser Ile Leu Ala Pro Ala Glu Tyr Asp Gln Asp Asn Ile Thr
130 135 140

Ala Leu Leu Asp Asp Ile Ser Lys Met Glu Ser Thr Gln Leu Ala Thr
145 150 155 160

Ser Pro Gly Thr Ser Tyr Leu Thr Ala Tyr Gln Ser Met Leu Asn Gly
165 170 175

Glu Ser Gln Ala Met Val Phe Asn Gly Val Phe Thr Asn Ile Leu Glu
180 185 190

Asn Glu Asp Pro Gly Phe Ser Ser Lys Val Lys Lys Ile Tyr Ser Phe
195 200 205

Lys Val Thr Gln Thr Val Glu Thr Ala Thr Lys Gln Val Ser Gly Asp
210 215 220

Ser Phe Asn Ile Tyr Ile Ser Gly Ile Asp Ala Tyr Gly Pro Ile Ser
225 230 235 240

Thr Val Ser Arg Ser Asp Val Asn Ile Ile Met Thr Val Asn Arg Ala
245 250 255

Thr His Lys Ile Leu Leu Thr Thr Thr Pro Arg Asp Ser Tyr Val Ala
260 265 270

Phe Ala Asp Gly Gly Gln Asn Gln Tyr Asp Lys Leu Thr His Ala Gly
275 280 285

Ile Tyr Gly Val Asn Ala Ser Val His Thr Leu Glu Asn Phe Tyr Gly
290 295 300

Ile Asp Ile Ser Asn Tyr Val Arg Leu Asn Phe Ile Ser Phe Leu Gln
305 310 315 320

Leu Ile Asp Leu Val Gly Gly Ile Asp Val Tyr Asn Asp Gln Glu Phe
325 330 335

Thr Ser Leu His Gly Asn Tyr His Phe Pro Val Gly Gln Val His Leu
340 345 350

Asn Ser Asp Gln Ala Leu Gly Phe Val Arg Glu Arg Tyr Ser Leu Thr
355 360 365

Gly Gly Asp Asn Asp Arg Gly Lys Asn Gln Glu Lys Val Ile Ala Ala
370 375 380

Leu Ile Lys Lys Met Ser Thr Pro Glu Asn Leu Lys Asn Tyr Gln Ala
385 390 395 400

Ile Leu Ser Gly Leu Glu Gly Ser Ile Gln Thr Asp Leu Ser Leu Glu
405 410 415

Thr Ile Met Ser Leu Val Asn Thr Gln Leu Glu Ser Gly Thr Gln Phe
420 425 430

Thr Val Glu Ser Gln Ala Leu Thr Gly Thr Gly Arg Ser Asp Leu Ser
435 440 445

Ser Tyr Ala Met Pro Gly Ser Gln Leu Tyr Met Met Glu Ile Asn Gln
450 455 460

Asp Ser Leu Glu Gln Ser Lys Ala Ala Ile Gln Ser Val Leu Val Glu
465 470 475 480

Lys

<210> 13

<211> 229

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS2B

<400> 13

Met Asn Asn Gln Glu Val Asn Ala Ile Glu Ile Asp Val Leu Phe Leu
1 5 10 15

Leu Lys Thr Ile Trp Arg Lys Lys Phe Leu Ile Leu Leu Thr Ala Val
20 25 30

Leu Thr Ala Gly Leu Ala Phe Val Tyr Ser Ser Phe Leu Val Thr Pro
35 40 45

Gln Tyr Asp Ser Thr Thr Arg Ile Tyr Val Val Ser Gln Asn Val Glu
50 55 60

Ala Gly Ala Gly Leu Thr Asn Gln Glu Leu Gln Ala Gly Thr Tyr Leu
65 70 75 80

Ala Lys Asp Tyr Arg Glu Ile Ile Leu Ser Gln Asp Val Leu Thr Gln
85 90 95

Val Ala Thr Glu Leu Asn Leu Lys Glu Ser Leu Lys Glu Lys Ile Ser
100 105 110

Val Ser Ile Pro Val Asp Thr Arg Ile Val Ser Ile Ser Val Arg Asp
115 120 125

Ala Asp Pro Asn Glu Ala Ala Arg Ile Ala Asn Ser Leu Arg Thr Phe
130 135 140

Ala Val Gln Lys Val Val Glu Val Thr Lys Val Ser Asp Val Thr Thr
145 150 155 160

Leu Glu Glu Ala Val Pro Ala Glu Glu Pro Thr Thr Pro Asn Thr Lys
165 170 175

Arg Asn Ile Leu Leu Gly Leu Leu Ala Gly Gly Ile Leu Ala Thr Gly
180 185 190

Leu Val Leu Val Met Glu Val Leu Asp Asp Arg Val Lys Arg Pro Gln
195 200 205

Asp Ile Glu Glu Val Met Gly Leu Thr Leu Leu Gly Ile Val Pro Asp
210 215 220

Ser Lys Lys Leu Lys
225

<210> 14

<211> 225

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS2C

<400> 14

Met Ala Met Leu Glu Ile Ala Arg Thr Lys Arg Glu Gly Val Asn Lys
1 5 10 15

Thr Glu Glu Tyr Phe Asn Ala Ile Arg Thr Asn Ile Gln Leu Ser Gly
20 25 30

Ala Asp Ile Lys Val Val Gly Ile Thr Ser Val Lys Ser Asn Glu Gly
35 40 45

Lys Ser Thr Thr Ala Ala Ser Leu Ala Ile Ala Tyr Ala Arg Ser Gly
50 55 60

Tyr Lys Thr Val Leu Val Asp Ala Asp Ile Arg Asn Ser Val Met Pro
65 70 75 80

Gly Phe Phe Lys Pro Ile Thr Lys Ile Thr Gly Leu Thr Asp Tyr Leu
85 90 95

Ala Gly Thr Thr Asp Leu Ser Gln Gly Leu Cys Asp Thr Asp Ile Pro
100 105 110

Asn Leu Thr Val Ile Glu Ser Gly Lys Val Ser Pro Asn Pro Thr Ala
115 120 125

Leu Leu Gln Ser Lys Asn Phe Glu Asn Leu Leu Ala Thr Leu Arg Arg
130 135 140

Tyr Tyr Asp Tyr Val Ile Val Asp Cys Pro Pro Leu Gly Leu Val Ile
145 150 155 160

Asp Ala Ala Ile Ile Ala Gln Lys Cys Asp Ala Met Val Ala Val Val
165 170 175

Glu Ala Gly Asn Val Lys Cys Ser Ser Leu Lys Lys Val Lys Glu Gln
180 185 190

Leu Glu Gln Thr Gly Thr Pro Phe Leu Gly Val Ile Leu Asn Lys Tyr
195 200 205

Asp Ile Ala Thr Glu Lys Tyr Ser Glu Tyr Gly Asn Tyr Gly Lys Lys
210 215 220

Ala
225

<210> 15

<211> 243

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS2D

<400> 15

Met Ile Asp Ile His Ser His Ile Ile Phe Gly Val Asp Asp Gly Pro
1 5 10 15

Lys Thr Ile Glu Glu Ser Leu Ser Leu Ile Ser Glu Ala Tyr Arg Gln
20 25 30

Gly Val Arg Tyr Ile Val Ala Thr Ser His Arg Arg Lys Gly Met Phe
35 40 45

Glu Thr Pro Glu Lys Ile Ile Met Ile Asn Phe Leu Gln Leu Lys Glu
50 55 60

Ala Val Ala Glu Val Tyr Pro Glu Ile Arg Leu Cys Tyr Gly Ala Glu
65 70 75 80

Leu Tyr Tyr Ser Lys Asp Ile Leu Ser Lys Leu Glu Lys Lys Lys Val
85 90 95

Pro Thr Leu Asn Gly Ser Cys Tyr Ile Leu Leu Glu Phe Ser Thr Asp
100 105 110

Thr Pro Trp Lys Glu Ile Gln Glu Ala Val Asn Glu Met Thr Leu Leu
115 120 125

Gly Leu Thr Pro Val Leu Ala His Ile Glu Arg Tyr Asp Ala Leu Ala
130 135 140

Phe Gln Ser Glu Arg Val Glu Lys Leu Ile Asp Lys Gly Cys Tyr Thr
145 150 155 160

Gln Val Asn Ser Asn His Val Leu Lys Pro Ala Leu Ile Gly Glu Arg
165 170 175

Ala Lys Glu Phe Lys Lys Arg Thr Arg Tyr Phe Leu Glu Gln Asp Leu
180 185 190

Val His Cys Val Ala Ser Asp Met His Asn Leu Tyr Ser Arg Pro Pro
195 200 205

Phe Met Arg Glu Ala Tyr Gln Leu Val Lys Lys Glu Tyr Gly Glu Asp
210 215 220

Arg Ala Lys Ala Leu Phe Lys Lys Asn Pro Leu Leu Ile Leu Lys Asn
225 230 235 240

Gln Val Gln

<210> 16

<211> 459

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS2E

<400> 16

Met Asn Ile Glu Ile Gly Tyr Arg Gln Thr Lys Leu Ala Leu Phe Asp
1 5 10 15

Met Ile Ala Val Thr Ile Ser Ala Ile Leu Thr Ser His Ile Pro Asn
20 25 30

Ala Asp Leu Asn Arg Ser Gly Ile Phe Ile Ile Met Met Val His Tyr
35 40 45

Phe Ala Phe Phe Ile Ser Arg Met Pro Val Glu Phe Glu Tyr Arg Gly
50 55 60

Asn Leu Ile Glu Phe Glu Lys Thr Phe Asn Tyr Ser Ile Ile Phe Val
65 70 75 80

Ile Phe Leu Met Ala Val Ser Phe Met Leu Glu Asn Asn Phe Ala Leu
85 90 95

Ser Arg Arg Gly Ala Val Tyr Phe Thr Leu Ile Asn Phe Val Leu Val
100 105 110

Tyr Leu Phe Asn Val Ile Ile Lys Gln Phe Lys Asp Ser Phe Leu Phe
115 120 125

Ser Thr Thr Tyr Gln Lys Lys Thr Ile Leu Ile Thr Thr Ala Glu Leu
130 135 140

Trp Glu Asn Met Gln Val Leu Phe Glu Ser Asp Ile Leu Phe Gln Lys
145 150 155 160

Asn Leu Val Ala Leu Val Ile Leu Gly Thr Glu Ile Asp Lys Ile Asn
165 170 175

Leu Pro Leu Pro Leu Tyr Tyr Ser Val Glu Glu Ala Ile Gly Phe Ser
180 185 190

Thr Arg Glu Val Val Asp Tyr Val Phe Ile Asn Leu Pro Ser Glu Tyr
195 200 205

Phe Asp Leu Lys Gln Leu Val Ser Asp Phe Glu Leu Leu Gly Ile Asp
210 215 220

Val Gly Val Asp Ile Asn Ser Phe Gly Phe Thr Val Leu Lys Asn Lys
225 230 235 240

Lys Ile Gln Met Leu Gly Asp His Ser Ile Val Thr Phe Ser Thr Asn
245 250 255

Phe Tyr Lys Pro Ser His Ile Trp Met Lys Arg Leu Leu Asp Ile Leu
260 265 270

Gly Ala Val Val Gly Leu Ile Ile Ser Gly Ile Val Ser Ile Leu Leu
275 280 285

Ile Pro Ile Ile Arg Arg Asp Gly Gly Pro Ala Ile Phe Ala Gln Lys
290 295 300

Arg Val Gly Gln Asn Gly Arg Ile Phe Thr Phe Tyr Lys Phe Arg Ser
305 310 315 320

Met Phe Val Asp Ala Glu Val Arg Lys Lys Glu Leu Met Ala Gln Asn
325 330 335

Gln Met Gln Gly Gly Met Phe Lys Met Asp Asn Asp Pro Arg Ile Thr
340 345 350

Pro Ile Gly His Phe Ile Arg Lys Thr Ser Leu Asp Glu Leu Pro Gln
355 360 365

Phe Tyr Asn Val Leu Ile Gly Asp Met Ser Leu Val Gly Thr Arg Pro
370 375 380

Pro Thr Val Asp Glu Phe Glu Lys Tyr Thr Pro Ser Gln Lys Arg Arg
385 390 395 400

Leu Ser Phe Lys Pro Gly Ile Thr Gly Leu Trp Gln Val Ser Gly Arg
405 410 415

Ser Asp Ile Thr Asp Phe Asn Glu Val Val Arg Leu Asp Leu Thr Tyr
420 425 430

Ile Asp Asn Trp Thr Ile Trp Ser Asp Ile Lys Ile Leu Leu Lys Thr
435 440 445

Val Lys Val Val Leu Leu Arg Glu Gly Gly Gln
450 455

<210> 17

<211> 389

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS2F

<400> 17

Met Arg Thr Val Tyr Ile Ile Gly Ser Lys Gly Ile Pro Ala Lys Tyr
1 5 10 15

Gly Gly Phe Glu Thr Phe Val Glu Lys Leu Thr Glu Tyr Gln Lys Asp
20 25 30

Lys Ser Ile Asn Tyr Phe Val Ala Cys Thr Arg Glu Asn Ser Ala Lys
35 40 45

Ser Asp Ile Thr Gly Glu Val Phe Glu His Asn Gly Ala Thr Cys Phe
50 55 60

Asn Ile Asp Val Pro Asn Ile Gly Ser Ala Lys Ala Ile Leu Tyr Asp
65 70 75 80

Ile Met Ala Leu Lys Lys Ser Ile Glu Ile Ala Lys Asp Arg Asn Asp
85 90 95

Thr Ser Pro Ile Phe Tyr Ile Leu Ala Cys Arg Ile Gly Pro Phe Ile
100 105 110

Tyr Leu Phe Lys Lys Gln Ile Glu Ser Ile Gly Gly Gln Leu Phe Val
115 120 125

Asn Pro Asp Gly His Glu Trp Leu Arg Glu Lys Trp Ser Tyr Pro Val
130 135 140

Arg Gln Tyr Trp Lys Phe Ser Glu Ser Leu Met Leu Lys Tyr Ala Asp
145 150 155 160

Leu Leu Ile Cys Asp Ser Lys Asn Ile Glu Lys Tyr Ile His Glu Asp
165 170 175

Tyr Arg Lys Tyr Ala Pro Glu Thr Ser Tyr Ile Ala Tyr Gly Thr Asp
180 185 190

Leu Asp Lys Ser Arg Leu Ser Pro Thr Asp Ser Val Val Arg Glu Trp
195 200 205

Tyr Lys Glu Lys Glu Ile Ser Glu Asn Asp Tyr Tyr Leu Val Val Gly
210 215 220

Arg Phe Val Pro Glu Asn Asn Tyr Glu Val Met Ile Arg Glu Phe Met
225 230 235 240

Lys Ser Tyr Ser Arg Lys Asp Phe Val Leu Ile Thr Asn Val Glu His
245 250 255

Asn Ser Phe Tyr Glu Lys Leu Lys Lys Glu Thr Gly Phe Asp Lys Asp
260 265 270

Lys Arg Ile Lys Phe Val Gly Thr Val Tyr Asn Gln Glu Leu Leu Lys
275 280 285

Tyr Ile Arg Glu Asn Ala Phe Ala Tyr Phe His Gly His Glu Val Gly
290 295 300

Gly Thr Asn Pro Ser Leu Leu Glu Ala Leu Ser Ser Thr Lys Leu Asn
305 310 315 320

Leu Leu Leu Asp Val Gly Phe Asn Arg Glu Val Gly Glu Glu Gly Ala
325 330 335

Lys Tyr Trp Asn Lys Asp Asn Leu His Arg Val Ile Asp Ser Cys Glu
340 345 350

Gln Leu Ser Gln Glu Gln Ile Asn Asp Met Asp Ser Leu Ser Thr Lys
355 360 365

Gln Val Lys Glu Arg Phe Ser Trp Asp Phe Ile Val Asp Glu Tyr Glu
370 375 380

Lys Leu Phe Lys Gly
385

<210> 18

<211> 385

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS2G

<400> 18

Met Lys Lys Ile Leu Tyr Leu His Ala Gly Ala Glu Leu Tyr Gly Ala
1 5 10 15

Asp Lys Val Leu Leu Glu Leu Ile Lys Gly Leu Asp Lys Asn Glu Phe
20 25 30

Glu Ala His Val Ile Leu Pro Asn Asp Gly Val Leu Val Pro Ala Leu
35 40 45

Arg Glu Val Gly Ala Gln Val Glu Val Ile Asn Tyr Pro Ile Leu Arg
50 55 60

Arg Lys Tyr Phe Asn Pro Lys Gly Ile Phe Asp Tyr Phe Ile Ser Tyr
65 70 75 80

His His Tyr Ser Lys Gln Ile Ala Gln Tyr Ala Ile Glu Asn Lys Val
85 90 95

Asp Ile Ile His Asn Asn Thr Thr Ala Val Leu Glu Gly Ile Tyr Leu
100 105 110

Lys Arg Lys Leu Lys Leu Pro Leu Leu Trp His Val His Glu Ile Ile
115 120 125

Val Lys Pro Lys Phe Ile Ser Asp Ser Ile Asn Phe Leu Met Gly Arg
130 135 140

Phe Ala Asp Lys Ile Val Thr Val Ser Gln Ala Val Ala Asn His Ile
145 150 155 160

Lys Gln Ser Pro His Ile Lys Asp Asp Gln Ile Ser Val Ile Tyr Asn
165 170 175

Gly Val Asp Asn Lys Val Phe Tyr Gln Ser Asp Ala Arg Ser Val Arg
180 185 190

Glu Arg Phe Asp Ile Asp Glu Glu Ala Leu Val Ile Gly Met Val Gly
195 200 205

Arg Val Asn Ala Trp Lys Gly Gln Gly Asp Phe Leu Glu Ala Val Ala
210 215 220

Pro Ile Leu Glu Gln Asn Pro Lys Ala Ile Ala Phe Ile Ala Gly Ser
225 230 235 240

Ala Phe Glu Gly Glu Glu Trp Arg Val Val Glu Leu Glu Lys Lys Ile
245 250 255

Ser Gln Leu Lys Val Ser Ser Gln Val Arg Arg Met Asp Tyr Tyr Ala
260 265 270

Asn Thr Thr Glu Leu Tyr Asn Met Phe Asp Ile Phe Val Leu Pro Ser
275 280 285

Thr Asn Pro Asp Pro Leu Pro Thr Val Val Leu Lys Ala Met Ala Cys
290 295 300

Gly Lys Pro Val Val Gly Tyr Arg His Gly Gly Val Cys Glu Met Val
305 310 315 320

Lys Glu Gly Val Asn Gly Phe Leu Val Thr Pro Asn Ser Pro Leu Asn
325 330 335

Leu Ser Lys Val Ile Leu Gln Leu Ser Glu Asn Ile Asn Leu Arg Lys
340 345 350

Lys Ile Gly Asn Asn Ser Ile Glu Arg Gln Lys Glu His Phe Ser Leu
355 360 365

Lys Ser Tyr Val Lys Asn Phe Ser Lys Val Tyr Thr Ser Leu Lys Val
370 375 380

Tyr
385

<210> 19

<211> 456

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> cps2h

<400> 19

Met Lys Ile Ile Ser Phe Thr Met Val Asn Asn Glu Ser Glu Ile Ile
1 5 10 15

Glu Ser Phe Ile Arg Tyr Asn Tyr Asn Phe Ile Asp Glu Met Val Ile
20 25 30

Ile Asp Asn Gly Cys Thr Asp Asn Thr Met Gln Ile Ile Phe Asn Leu
35 40 45

Ile Lys Glu Gly Tyr Lys Ile Ser Val Tyr Asp Glu Ser Leu Glu Ala
50 55 60

Tyr Asn Gln Tyr Arg Leu Asp Asn Lys Tyr Leu Thr Lys Ile Ile Ala
65 70 75 80

Glu Lys Asn Pro Asp Leu Ile Ile Pro Leu Asp Ala Asp Glu Phe Leu
85 90 95

Thr Ala Asp Ser Asn Pro Arg Lys Leu Leu Glu Gln Leu Asp Leu Glu
100 105 110

Lys Ile His Tyr Val Asn Trp Gln Trp Phe Val Met Thr Lys Lys Asp
115 120 125

Asp Ile Asn Asp Ser Phe Ile Pro Arg Arg Met Gln Tyr Cys Phe Glu
130 135 140

Lys Pro Val Trp His His Ser Asp Gly Lys Pro Val Thr Lys Cys Ile
145 150 155 160

Ile Ser Ala Lys Tyr Tyr Lys Lys Met Asn Leu Lys Leu Ser Met Gly
165 170 175

His His Thr Val Phe Gly Asn Pro Asn Val Arg Ile Glu His His Asn
180 185 190

Asp Leu Lys Phe Ala His Tyr Arg Ala Ile Ser Gln Glu Gln Leu Ile
195 200 205

Tyr Lys Thr Ile Cys Tyr Thr Ile Arg Asp Ile Ala Thr Met Glu Asn
210 215 220

Asn Ile Glu Thr Ala Gln Arg Thr Asn Gln Met Ala Leu Ile Glu Ser
225 230 235 240

Gly Val Asp Met Trp Glu Thr Ala Arg Glu Ala Ser Tyr Ser Gly Tyr
245 250 255

Asp Cys Asn Val Ile His Ala Pro Ile Asp Leu Ser Phe Cys Lys Glu
260 265 270

Asn Ile Val Ile Lys Tyr Asn Glu Leu Ser Arg Glu Thr Val Ala Glu
275 280 285

Arg Val Met Lys Thr Gly Arg Glu Met Ala Val Arg Ala Tyr Asn Val
290 295 300

Glu Arg Lys Gln Lys Glu Lys Lys Phe Leu Lys Pro Ile Ile Phe Val
305 310 315 320

Leu Asp Gly Leu Lys Gly Asp Glu Tyr Ile His Pro Asn Pro Ser Asn
325 330 335

His Leu Thr Ile Leu Thr Glu Met Tyr Asn Val Arg Gly Leu Leu Thr
340 345 350

Asp Asn His Gln Ile Lys Phe Leu Lys Val Asn Tyr Arg Leu Ile Ile
355 360 365

Thr Pro Asp Phe Ala Lys Phe Leu Pro His Glu Phe Ile Val Val Pro
370 375 380

Asp Thr Leu Asp Ile Glu Gln Val Lys Ser Gln Tyr Val Gly Thr Gly
385 390 395 400

Val Asp Leu Ser Lys Ile Ile Ser Leu Lys Glu Tyr Arg Lys Glu Ile
405 410 415

Gly Phe Ile Gly Asn Leu Tyr Ala Leu Leu Gly Phe Val Pro Asn Met
420 425 430

Leu Asn Arg Ile Tyr Leu Tyr Ile Gln Arg Asn Gly Ile Ala Asn Thr
435 440 445

Ile Ile Lys Ile Lys Ser Arg Leu
450 455

<210> 20

<211> 410

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS2I

<400> 20

Met Gln Ala Asp Arg Arg Lys Thr Phe Gly Lys Met Arg Ile Arg Ile
1 5 10 15

Asn Asn Leu Phe Phe Val Ala Ile Ala Phe Met Gly Ile Ile Ile Ser
20 25 30

Asn Ser Gln Val Val Leu Ala Ile Gly Lys Ala Ser Val Ile Gln Tyr
35 40 45

Leu Ser Tyr Leu Val Leu Ile Leu Cys Ile Val Asn Asp Leu Leu Lys
50 55 60

Asn Asn Lys His Ile Val Val Tyr Lys Leu Gly Tyr Leu Phe Leu Ile
65 70 75 80

Ile Phe Leu Phe Thr Ile Gly Ile Cys Gln Gln Ile Leu Pro Ile Thr
85 90 95

Thr Lys Ile Tyr Leu Ser Ile Ser Met Met Ile Ile Ser Val Leu Ala
100 105 110

Thr Leu Pro Ile Ser Leu Ile Lys Asp Ile Asp Asp Phe Arg Arg Ile
115 120 125

Ser Asn His Leu Leu Phe Ala Leu Phe Ile Thr Ser Ile Leu Gly Ile
130 135 140

Lys Met Gly Ala Thr Met Phe Thr Gly Ala Val Glu Gly Ile Gly Phe
145 150 155 160

Ser Gln Gly Phe Asn Gly Gly Leu Thr His Lys Asn Phe Phe Gly Ile
165 170 175

Thr Ile Leu Met Gly Phe Val Leu Thr Tyr Leu Ala Tyr Lys Tyr Gly
180 185 190

Ser Tyr Lys Arg Thr Asp Arg Phe Ile Leu Gly Leu Glu Leu Phe Leu
195 200 205

Ile Leu Ile Ser Asn Thr Arg Ser Val Tyr Leu Ile Leu Leu Leu Phe
210 215 220

Leu Phe Leu Val Asn Leu Asp Lys Ile Lys Ile Glu Gln Arg Gln Trp
225 230 235 240

Ser Thr Leu Lys Tyr Ile Ser Met Leu Phe Cys Ala Ile Phe Leu Tyr
245 250 255

Tyr Phe Phe Gly Phe Leu Ile Thr His Ser Asp Ser Tyr Ala His Arg
260 265 270

Val Asn Gly Leu Ile Asn Phe Phe Glu Tyr Tyr Arg Asn Asp Trp Phe
275 280 285

His Leu Met Phe Gly Ala Ala Asp Leu Ala Tyr Gly Asp Leu Thr Leu
290 295 300

Asp Tyr Ala Ile Arg Val Arg Arg Val Leu Gly Trp Asn Gly Thr Leu
305 310 315 320

Glu Met Pro Leu Leu Ser Ile Met Leu Lys Asn Gly Phe Ile Gly Leu
325 330 335

Val Gly Tyr Gly Ile Val Leu Tyr Lys Leu Tyr Arg Asn Val Arg Ile
340 345 350

Leu Lys Thr Asp Asn Ile Lys Thr Ile Gly Lys Ser Val Phe Ile Ile
355 360 365

Val Val Leu Ser Ala Thr Val Glu Asn Tyr Ile Val Asn Leu Ser Phe
370 375 380

Val Phe Met Pro Ile Cys Phe Cys Leu Leu Asn Ser Ile Ser Thr Met
385 390 395 400

Glu Ser Thr Ile Asn Lys Gln Leu Gln Thr
405 410

<210> 21

<211> 332

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS2J

<400> 21

Met Glu Lys Val Ser Ile Ile Val Pro Ile Phe Asn Thr Glu Lys Tyr
1 5 10 15

Leu Arg Glu Cys Leu Asp Ser Ile Ile Ser Gln Ser Tyr Thr Asn Leu
20 25 30

Glu Ile Leu Leu Ile Asp Asp Gly Ser Ser Asp Ser Ser Thr Asp Ile
35 40 45

Cys Leu Glu Tyr Ala Glu Gln Asp Gly Arg Ile Lys Leu Phe Arg Leu
50 55 60

Pro Asn Gly Gly Val Ser Asn Ala Arg Asn Tyr Gly Ile Lys Asn Ser
65 70 75 80

Thr Ala Asn Tyr Ile Met Phe Val Asp Ser Asp Asp Ile Val Asp Gly
85 90 95

Asn Ile Val Glu Ser Leu Tyr Thr Cys Leu Lys Glu Asn Asp Ser Asp
100 105 110

Leu Ser Gly Gly Leu Leu Ala Thr Phe Asp Gly Asn Tyr Gln Glu Ser
115 120 125

Glu Leu Gln Lys Cys Gln Ile Asp Leu Glu Glu Ile Lys Glu Val Arg
130 135 140

Asp Leu Gly Asn Glu Asn Phe Pro Asn His Tyr Met Ser Gly Ile Phe
145 150 155 160

Asn Ser Pro Cys Cys Lys Leu Tyr Lys Asn Ile Tyr Ile Asn Gln Gly
165 170 175

Phe Asp Thr Glu Gln Trp Leu Gly Glu Asp Leu Leu Phe Asn Leu Asn
180 185 190

Tyr Leu Lys Asn Ile Lys Lys Val Arg Tyr Val Asn Arg Asn Leu Tyr
195 200 205

Phe Ala Arg Arg Ser Leu Gln Ser Thr Thr Asn Thr Phe Lys Tyr Asp
210 215 220

Val Phe Ile Gln Leu Glu Asn Leu Glu Glu Lys Thr Phe Asp Leu Phe
225 230 235 240

Val Lys Ile Phe Gly Gly Gln Tyr Glu Phe Ser Val Phe Lys Glu Thr
245 250 255

Leu Gln Trp His Ile Ile Tyr Tyr Ser Leu Leu Met Phe Lys Asn Gly
260 265 270

Asp Glu Ser Leu Pro Lys Lys Leu His Ile Phe Lys Tyr Leu Tyr Asn
275 280 285

Arg His Ser Leu Asp Thr Leu Ser Ile Lys Arg Thr Ser Ser Val Phe
290 295 300

Lys Arg Ile Cys Lys Leu Ile Val Ala Asn Asn Leu Phe Lys Ile Phe
305 310 315 320

Leu Asn Thr Leu Ile Arg Glu Glu Lys Asn Asn Asp
325 330

<210> 22

<211> 332

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS2K

<400> 22

Met Ile Asn Ile Ser Ile Ile Val Pro Ile Tyr Asn Val Glu Gln Tyr
1 5 10 15

Leu Ser Lys Cys Ile Asn Ser Ile Val Asn Gln Thr Tyr Lys His Ile
20 25 30

Glu Ile Leu Leu Val Asn Asp Gly Ser Thr Asp Asn Ser Glu Glu Ile
35 40 45

Cys Leu Ala Tyr Ala Lys Lys Asp Ser Arg Ile Arg Tyr Phe Lys Lys
50 55 60

Glu Asn Gly Gly Leu Ser Asp Ala Arg Asn Tyr Gly Ile Ser Arg Ala
65 70 75 80

Lys Gly Asp Tyr Leu Ala Phe Ile Asp Ser Asp Asp Phe Ile His Ser
85 90 95

Glu Phe Ile Gln Arg Leu His Glu Ala Ile Glu Arg Glu Asn Ala Leu
100 105 110

Val Ala Val Ala Gly Tyr Asp Arg Val Asp Ala Ser Gly His Phe Leu
115 120 125

Thr Ala Glu Pro Leu Pro Thr Asn Gln Ala Val Leu Ser Gly Arg Asn
130 135 140

Val Cys Lys Lys Leu Leu Glu Ala Asp Gly His Arg Phe Val Val Ala
145 150 155 160

Trp Asn Lys Leu Tyr Lys Lys Glu Leu Phe Asp Phe Arg Phe Glu Lys
165 170 175

Gly Lys Ile His Glu Asp Glu Tyr Phe Thr Tyr Arg Leu Leu Tyr Glu
180 185 190

Leu Glu Lys Val Ala Ile Val Lys Glu Cys Leu Tyr Tyr Tyr Val Asp
195 200 205

Arg Glu Asn Ser Ile Ile Thr Ser Ser Met Thr Asp His Arg Phe His
210 215 220

Cys Leu Leu Glu Phe Gln Asn Glu Arg Met Asp Phe Tyr Glu Ser Arg
225 230 235 240

Gly Asp Lys Glu Leu Leu Leu Glu Cys Tyr Arg Ser Phe Leu Ala Phe
245 250 255

Ala Val Leu Phe Leu Gly Lys Tyr Asn His Trp Leu Ser Lys Gln Gln
260 265 270

Lys Lys Leu Gln Thr Leu Phe Arg Ile Val Tyr Lys Gln Leu Lys Gln
275 280 285

Asn Lys Arg Leu Ala Leu Leu Met Asn Ala Tyr Tyr Leu Val Gly Cys
290 295 300

Leu His Leu Asn Phe Ser Val Phe Leu Lys Thr Gly Lys Asp Lys Ile
305 310 315 320

Gln Glu Arg Leu Arg Arg Ser Glu Ser Ser Thr Arg
325 330

<210> 23

<211> 467

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS2O

<220>

<221> misc_feature

<222> (1)..(467)

<223> Xaa may be any amino acid

<400> 23

Met Ser Lys Lys Ser Ile Val Val Ser Gly Leu Val Tyr Thr Ile Gly
1 5 10 15

Thr Ile Leu Val Gln Gly Leu Ala Phe Ile Thr Leu Pro Ile Tyr Thr
20 25 30

Arg Val Ile Ser Gln Glu Val Tyr Gly Gln Phe Ser Leu Tyr Asn Ser
35 40 45

Trp Val Gly Leu Val Gly Leu Phe Ile Gly Leu Gln Leu Gly Gly Ala
50 55 60

Phe Gly Pro Gly Trp Val His Phe Arg Glu Lys Phe Asp Asp Phe Val
65 70 75 80

Ser Thr Leu Met Val Ser Ser Ile Ala Phe Phe Leu Pro Ile Phe Gly
85 90 95

Leu Ser Phe Leu Leu Ser Gln Pro Leu Ser Leu Leu Phe Gly Leu Pro
100 105 110

Asp Trp Val Val Pro Leu Ile Phe Leu Gln Ser Leu Met Ile Val Val
115 120 125

Gln Gly Phe Phe Thr Thr Tyr Leu Val Gln Arg Gln Gln Ser Met Trp
130 135 140

Thr Leu Pro Leu Ser Val Leu Ser Ala Val Ile Asn Thr Ala Leu Ser
145 150 155 160

Leu Phe Leu Thr Phe Pro Met Glu Asn Asp Phe Ile Ala Arg Val Met
165 170 175

Ala Asn Pro Ala Thr Thr Gly Val Leu Ala Cys Val Ser Xaa Trp Phe
180 185 190

Ser Gln Lys Lys Asn Gly Leu His Phe Arg Lys Asp Tyr Leu Arg Tyr
195 200 205

Gly Leu Ser Ile Ser Ile Pro Leu Ile Phe His Gly Leu Gly His Asn
210 215 220

Val Leu Asn Gln Phe Asp Arg Ile Met Leu Gly Lys Met Leu Thr Leu
225 230 235 240

Ser Asp Val Ala Leu Tyr Ser Phe Gly Tyr Thr Leu Ala Ser Ile Leu
245 250 255

Gln Ile Val Phe Ser Ser Leu Asn Thr Val Trp Cys Pro Trp Tyr Phe
260 265 270

Glu Lys Lys Arg Gly Ala Asp Lys Asp Leu Leu Ser Tyr Val Arg Tyr
275 280 285

Tyr Leu Ala Ile Gly Leu Phe Val Thr Phe Gly Phe Leu Thr Ile Tyr
290 295 300

Pro Arg Leu Ala Met Leu Leu Gly Gly Ser Glu Tyr Arg Phe Ser Met
305 310 315 320

Gly Phe Ile Pro Met Ile Ile Val Gly Val Phe Phe Val Phe Leu Tyr
325 330 335

Ser Phe Pro Ala Asn Ile Gln Phe Tyr Ser Gly Asn Thr Lys Phe Leu
340 345 350

Pro Ile Gly Thr Phe Ile Ala Gly Val Leu Asn Ile Ser Val His Phe
355 360 365

Val Leu Ile Pro Thr Lys Asn Leu Trp Cys Cys Phe Ala Thr Thr Ala
370 375 380

Ser Tyr Leu Leu Leu Leu Val Leu His Tyr Phe Val Ala Lys Lys Lys
385 390 395 400

Tyr Ala Tyr Asp Glu Val Ala Ile Ser Thr Phe Val Lys Val Ile Ala
405 410 415

Leu Val Val Val Tyr Thr Gly Leu Met Thr Val Phe Val Gly Ser Ile
420 425 430

Trp Ile Arg Trp Ser Leu Gly Ile Ala Val Leu Val Val Tyr Ala Ile
435 440 445

Tyr Phe Arg Lys Glu Leu Thr Val Ala Leu Asn Thr Phe Arg Glu Lys
450 455 460

Arg Ser Lys
465

<210> 24

<211> 338

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS2P

<400> 24

Met Val Tyr Ile Ile Ala Glu Ile Gly Cys Asn His Asn Gly Asp Val
1 5 10 15

His Leu Ala Arg Lys Met Val Glu Val Ala Val Asp Cys Gly Val Asp
20 25 30

Ala Val Lys Phe Gln Thr Glu Lys Ala Asp Leu Leu Ile Ser Lys Tyr
35 40 45

Ala Pro Lys Ala Glu Tyr Gln Lys Ile Thr Thr Gly Glu Ser Asp Ser
50 55 60

Gln Leu Glu Met Thr Arg Arg Leu Glu Leu Ser Phe Glu Glu Tyr Leu
65 70 75 80

Asp Leu Arg Asp Tyr Cys Leu Glu Lys Gly Val Asp Val Phe Ser Thr
85 90 95

Pro Glu Asp Glu Glu Ser Leu Asp Phe Leu Ile Ser Thr Asp Met Pro
100 105 110

Val Tyr Lys Ile Pro Ser Gly Glu Ile Thr Asn Leu Pro Tyr Leu Glu
115 120 125

Lys Ile Gly Arg Gln Ala Lys Lys Val Ile Leu Ser Thr Gly Met Ala
130 135 140

Val Met Asp Glu Ile His Gln Ala Val Lys Ile Leu Gln Glu Asn Gly
145 150 155 160

Thr Thr Asp Ile Ser Ile Leu His Cys Thr Thr Glu Tyr Pro Thr Pro
165 170 175

Tyr Pro Ala Leu Asn Leu Asn Val Leu His Thr Leu Lys Lys Glu Phe
180 185 190

Pro Asn Leu Thr Ile Gly Tyr Ser Asp His Ser Val Gly Ser Glu Val
195 200 205

Pro Ile Ala Ala Ala Ala Met Gly Ala Glu Leu Ile Glu Lys His Phe
210 215 220

Thr Leu Asp Asn Glu Met Glu Gly Pro Asp His Lys Ala Ser Ala Thr
225 230 235 240

Pro Asp Ile Leu Ala Ala Leu Val Lys Gly Val Arg Ile Val Glu Gln
245 250 255

Ser Leu Gly Lys Phe Glu Lys Glu Pro Glu Glu Val Glu Val Arg Asn
260 265 270

Lys Ile Val Ala Glu Lys Ser Ile Val Ala Lys Lys Ala Ile Ala Lys
275 280 285

Gly Glu Val Phe Thr Glu Glu Asn Ile Thr Val Lys Arg Pro Gly Asn
290 295 300

Gly Ile Ser Pro Met Glu Trp Tyr Lys Val Leu Gly Gln Val Ser Glu
305 310 315 320

Gln Asp Phe Glu Glu Asp Gln Asn Ile Cys His Ser Ala Phe Glu Asn
325 330 335

Gln Met

<210> 25

<211> 170

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS2Q

<400> 25

Met Lys Lys Ile Cys Phe Val Thr Gly Ser Arg Ala Glu Tyr Gly Ile
1 5 10 15

Met Arg Arg Leu Leu Ser Tyr Leu Gln Asp Asp Pro Glu Met Glu Leu
20 25 30

Asp Leu Val Val Ala Thr Met His Leu Glu Glu Lys Tyr Gly Met Thr
35 40 45

Val Lys Asp Ile Glu Ala Asp Lys Arg Arg Ile Val Lys Arg Ile Pro
50 55 60

Leu His Leu Thr Asp Thr Ser Lys Gln Thr Ile Val Lys Ser Leu Ala
65 70 75 80

Thr Leu Thr Glu Gln Leu Thr Val Leu Phe Glu Glu Val Gln Tyr Asp
85 90 95

Leu Val Leu Ile Leu Gly Asp Arg Tyr Glu Met Leu Pro Val Ala Asn
100 105 110

Ala Ala Leu Leu Tyr Asn Ile Pro Ile Cys His Ile His Gly Gly Glu
115 120 125

Lys Thr Met Gly Asn Phe Asp Glu Ser Ile Arg His Ala Ile Thr Lys
130 135 140

Met Ser His Leu His Leu Thr Ser Thr Asp Glu Phe Arg Asn Arg Val
145 150 155 160

Ile Gln Leu Gly Glu Asn Pro Thr Met Tyr
165 170

<210> 26

<211> 184

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS2R

<400> 26

Met Glu Leu Gly Ile Asp Phe Ala Glu Asp Tyr Tyr Val Val Leu Phe
1 5 10 15

His Pro Val Thr Leu Glu Asp Asn Thr Ala Glu Glu Gln Thr Gln Ala
20 25 30

Leu Leu Asp Ala Leu Lys Glu Asp Gly Ser Gln Cys Leu Ile Ile Gly
35 40 45

Ser Asn Ser Asp Thr His Ala Asp Lys Ile Met Glu Leu Met His Glu
50 55 60

Phe Val Lys Gln Asp Ser Asp Ser Tyr Ile Phe Thr Ser Leu Pro Thr
65 70 75 80

Arg Tyr Tyr His Ser Leu Val Lys His Ser Gln Gly Leu Ile Gly Asn
85 90 95

Ser Ser Ser Gly Leu Ile Glu Val Pro Ser Leu Gln Val Pro Thr Leu
100 105 110

Asn Ile Gly Asn Arg Gln Phe Gly Arg Leu Ser Gly Pro Ser Val Val
115 120 125

His Val Gly Thr Ser Lys Glu Ala Ile Val Gly Gly Leu Gly Gln Leu
130 135 140

Arg Asp Val Ile Asp Phe Thr Asn Pro Phe Glu Gln Pro Asp Ser Ala
145 150 155 160

Leu Gln Gly Tyr Arg Ala Ile Lys Glu Phe Leu Ser Val Gln Ala Ser
165 170 175

Thr Met Lys Glu Phe Tyr Asp Arg
180

<210> 27

<211> 208

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS2S

<400> 27

Met Lys Lys Val Ala Phe Leu Gly Ala Gly Thr Phe Ser Asp Gly Val
1 5 10 15

Leu Pro Trp Leu Asp Arg Thr Arg Tyr Glu Leu Ile Gly Tyr Phe Glu
20 25 30

Asp Lys Pro Ile Ser Asp Tyr Arg Gly Tyr Pro Val Phe Gly Pro Leu
35 40 45

Gln Asp Val Leu Thr Tyr Leu Asp Asp Gly Lys Val Asp Ala Val Phe
50 55 60

Val Thr Ile Gly Asp Asn Val Lys Arg Lys Glu Ile Phe Asp Leu Leu
65 70 75 80

Ala Lys Asp His Tyr Asp Ala Leu Phe Asn Ile Ile Ser Glu Gln Ala
85 90 95

Asn Ile Phe Ser Pro Asp Ser Ile Lys Gly Arg Gly Val Phe Ile Gly
100 105 110

Phe Ser Ser Phe Val Gly Ala Asp Ser Tyr Val Tyr Asp Asn Cys Ile
115 120 125

Ile Asn Thr Gly Ala Ile Val Glu His His Thr Thr Val Glu Ala His
130 135 140

Cys Asn Ile Thr Pro Gly Val Thr Ile Asn Gly Leu Cys Arg Ile Gly
145 150 155 160

Glu Ser Thr Tyr Ile Gly Ser Gly Ser Thr Val Ile Gln Cys Ile Glu
165 170 175

Ile Ala Pro Tyr Thr Thr Leu Gly Ala Gly Thr Val Val Leu Lys Ser
180 185 190

Leu Thr Glu Ser Gly Thr Tyr Val Gly Val Pro Ala Arg Lys Ile Lys
195 200 205

<210> 28

<211> 410

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS2T

<400> 28

Met Glu Pro Ile Cys Leu Ile Pro Ala Arg Ser Gly Ser Lys Gly Leu
1 5 10 15

Pro Asn Lys Asn Met Leu Phe Leu Asp Gly Val Pro Met Ile Phe His
20 25 30

Thr Ile Arg Ala Ala Ile Glu Ser Gly Cys Phe Lys Lys Glu Asn Ile
35 40 45

Tyr Val Ser Thr Asp Ser Glu Val Tyr Lys Glu Ile Cys Glu Thr Thr
50 55 60

Gly Val Gln Val Leu Met Arg Pro Ala Asp Leu Ala Thr Asp Phe Thr
65 70 75 80

Thr Ser Phe Gln Leu Asn Glu His Phe Leu Gln Asp Phe Ser Asp Asp
85 90 95

Gln Val Phe Val Leu Leu Gln Val Thr Ser Pro Leu Arg Ser Gly Lys
100 105 110

His Val Lys Glu Ala Met Glu Leu Tyr Gly Lys Gly Gln Ala Asp His
115 120 125

Val Val Ser Phe Thr Lys Val Asp Lys Ser Pro Thr Leu Phe Ser Thr
130 135 140

Leu Asp Glu Asn Gly Phe Ala Lys Asp Ile Ala Gly Leu Gly Gly Ser
145 150 155 160

Tyr Arg Arg Gln Asp Glu Lys Thr Leu Tyr Tyr Pro Asn Gly Ala Ile
165 170 175

Tyr Ile Ser Ser Lys Gln Ala Tyr Leu Ala Asp Lys Thr Tyr Phe Ser
180 185 190

Glu Lys Thr Ala Ala Tyr Val Met Thr Lys Glu Asp Ser Ile Asp Val
195 200 205

Asp Asp His Phe Asp Phe Thr Gly Val Ile Gly Arg Ile Tyr Phe Asp
210 215 220

Tyr Gln Arg Arg Glu Gln Gln Asn Lys Pro Phe Tyr Lys Arg Glu Leu
225 230 235 240

Lys Arg Leu Cys Glu Gln Arg Val His Asp Ser Leu Val Ile Gly Asp
245 250 255

Ser Arg Leu Leu Ala Leu Leu Leu Asp Gly Phe Asp Asn Ile Ser Ile
260 265 270

Gly Gly Met Thr Ala Ser Thr Ser Leu Glu Asn Gln Gly Leu Phe Leu
275 280 285

Ala Thr Pro Ile Lys Lys Val Leu Leu Ser Leu Gly Val Asn Asp Leu
290 295 300

Ile Thr Asp Tyr Pro Leu His Met Ile Glu Asp Thr Ile Arg Gln Leu
305 310 315 320

Met Glu Ser Leu Val Ser Lys Ala Glu Gln Val Glu Val Thr Thr Ile
325 330 335

Ala Tyr Thr Leu Phe Arg Asp Ser Val Ser Asn Glu Glu Thr Val Gln
340 345 350

Leu Asn Asp Val Ile Val Gln Ser Ala Ser Glu Leu Gly Ile Ser Val
355 360 365

Ile Asp Leu Asn Glu Val Val Glu Lys Glu Ala Met Leu Asp Tyr Gln
370 375 380

Tyr Thr Asn Asp Gly Leu His Phe Asn Gln Ile Gly Gln Glu Arg Val
385 390 395 400

Asn Gln Leu Ile Leu Thr Ser Leu Thr Arg
405 410

<210> 29

<211> 6992

<212> DNA

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS1

<400> 29

atcgccaaac gaaattggca ttatttgata tgatagcagt tgcaatttct gcaatcttaa 60

caagtcatat accaaatgct gatttaaatc gttctggaat ttttatcata atgatggttc 120

attattttgc atttttata tctcgtatgc cagttgaatt tgagtataga ggtaatctga 180

tagagtttga aaaaacattt aactatagta taatatttgc aatttttctt acggcagtat 240

cattttgtt ggagaataat ttcgcacttt caagacgtgg tgccgtgtat ttcacattaa 300

taaacttcgt tttggtatac ctatttaacg taattattaa gcagtttaag gatagctttc 360

tattttcgac aatctatcaa aaaaagacga ttctaattac aacggctgaa cgatgggaaa 420

atatgcaagt tttatttgaa tcacataaac aaattcaaaa aaatcttgtt gcattggtag 480

ttttaggtac agaaatagat aaaattaatt tatcattacc gctctattat tctgtggaag 540

aagctataga gttttcaaca agggaagtgg tcgaccacgt ctttataaat ctaccaagtg 600

agtttttaga cgtaaagcaa ttcgtttcag attttgagtt gttaggtatt gatgtaagcg 660

ttgatattaa ttcattcggt tttactgcgt tgaaaaacaa aaaaatccaa ctgctaggtg 720

accatagcat tgtaactttt tccacaaatt tttataagcc tagtcatatc atgatgaaac 780

gacttttgga tatactcgga gcggtagtcg ggttaattat ttgtggtata gtttctattt 840

tgttagttcc aattattcgt agagatggtg gaccggctat ttttgctcag aaacgagttg 900

gacagaatgg acgcatattt acattctaca agtttcgatc gatgtatgtt gatgctgagg 960

agcgcaaaaa agacttgctc agccaaaacc agatgcaagg gtgggtatgt tttaaaatgg 1020

gaaaaacgat cctagaatta ctccaattgg acatttcata cgcaaaaaca agtttagacg 1080

agttaccaca gttttataat gttttaattg gcgatatgag tctagttggt acacgtccac 1140

ctacagttga tgaatttgaa aaatatactc ctggtcaaaa gagacgattg agttttaaac 1200

cagggattac aggtctctgg caggttagtg gtcgtagtaa tatcacagac ttcgacgacg 1260

tagttcggtt ggacttagca tacattgata attggactat ctggtcagat attaaaattt 1320

tattaaagac agtgaaagtt gtattgttga gagagggaag taagtaaaag tatatgaaag 1380

tttgtttggt cggttcttca gggggacatt tgactcactt gtatttgtta aaaccgtttt 1440

ggaaggaaga agaacgtttt tgggtaacat ttgataaaga ggatgcaaga agtcttttga 1500

agaatgaaaa aatgtatcca tgttactttc caacaaatcg caatctcatt aatttagtga 1560

aaaatacttt cttagctttc aaaattttac gtgatgagaa accagatgtt attatttcat 1620

ctggtgcggc cgttgctgtc cccttctttt acatcggaaa actatttgga gcaaagacga 1680

tttatattga agtatttgat cgagttaata aatctacatt aactggaaaa ctagtttatc 1740

ccgtaacaga tatttttatt gttcagtggg aagaaatgaa gaaggtatat cctaaatcta 1800

ttaacttggg gagtattttt taatgatttt tgtaacagta ggaactcatg aacaacagtt 1860

taatcgattg ataaaagaga ttgatttatt gaaaaaaaat ggaagtataa ccgacgaaat 1920

atttattcaa acaggatatt ctgactatat tccagaatat tgcaagtata aaaaatttct 1980

cagttacaaa gaaatggaac aatatattaa caaatcagaa gtagttattt gccacggagg 2040

ccccgctact tttatgaatt cattatccaa aggaaaaaaa caattattgt ttcctagaca 2100

aaaaaagtat ggtgaacatg taaatgatca tcaagtagag tttgtaagaa gaattttaca 2160

agataataat attttattta tagaaaatat agatgatttg tttgaaaaaa ttattgaagt 2220

ttctaagcaa actaacttta catcaaataa taatttttt tgtgaaagat taaaacaaat 2280

agttgaaaaa tttaatgagg atcaagaaaa tgaataataa aaaagatgca tatttgataa 2340

tggcttatca taatttttct cagattttac tggagaggga tacagatatt atcatcttct 2400

ctcaggagaa tgcacaccat tagttccttc agaatacctg tataattatt ttaaatattc 2460

tcaggattta tatgttgaat ttacaaaaga tgagcaaaaa tataaagaaa ataggatata 2520

tgaacgagtt aaatgttaca gattatttcc taatatatca gaaaaaacta ttgataatgt 2580

actgtttaga attttattaa gaatgtatcg agcttttgaa tactatttac aaagattgtt 2640

gtttattgat agaataaaaa acatggtcta agaataagat ttggttctaa ttgggtttcg 2700

cttccacatg attttgtggc aattctttta tcaaatgaaa acgaaacagc ttatttattt 2760

aagtaatcta aatgtccaga tgaactattt atacagacaa ttatagaaaa atatgaattt 2820

tcaaatagat tatctaaata tggaaattta agatatataa agtggaaaaa atcaacatct 2880

tctcctattg tctttacaga tgattctatt gatgaattgc taaatgcaag aaatttaggt 2940

tttttatttg ctagaaagtt aaaaatagaa aataaatcta aatttaaaga aattattact 3000

aaaaaataaa atagttgatt ttgtgagagt aatgtatgtt taaattattt aaatatgacc 3060

cggaatattt tatttttaag tacttctggt tgattatttt tattccagag caaaagtatg 3120

tatttttatt aatttttatg aatttaattt tatttcatat aaaatttttg aaaactaagc 3180

taatattaaa aaatgaaatt ttattgtttt tattatggtc tatattatgt tttgtttcag 3240

tagtcacaag tatgtttgtt gaaataaatt ttgaaagatt atttgcagat tttactgctc 3300

ccataatttg gattattgca ataatgtatt ataatttgta ttcatttata aatattgatt 3360

ataaaaaatt aaaaaatagt atctttttta gtttttttagt tttattaggt atatctgcat 3420

tgtatattat tcaaaatggg aaagatattg tatttttaga cagacacctt ataggactag 3480

actatcttat aacaggcgtc aaaacaaggt tggttggctt tatgaactat cctacgttaa 3540

ataccactac aattatagtt tcaattccgt taatctttgc acttataaaa aataaaatgc 3600

aacaattttt tttcttgtgt cttgctttta taccgatcta tttaagtgga tcgagaattg 3660

gtagtttatc gctagcaata ttaattatat gcttgttatg gagatatata ggtggaaaat 3720

ttgcttggat aaaaaagcta atagtaatat ttgtaatact acttattatt ttaaatactg 3780

aattgcttta ccatgaaatt ttggctgttt ataattctag agaatcaagt aacgaagcta 3840

gatttattat ttatcaagga agtattgata aagtattaga aaacaatatt ttatttggat 3900

atggaatatc cgaatattca gttacgggaa cttggctcgg aagtcattca ggctatatat 3960

cattttttta taaatcagga atagttgggt tgattttact gatgttttct tttttttatg 4020

ttataaaaaa aagttatgga gttaatgggg aaacagcact attttatttt acatcattag 4080

ccatattttt catatatgaa acaatagatc cgattattat tatattagta ctattctttt 4140

cttcaatagg tatttggaat aatataaatt ttaaaaagga tatggagaca aaaaatgaat 4200

gatttaattt cagttattgt accaatttat aatgtccaag attatcttga taaatgtatt 4260

aacagtatta ttaaccaaac atatactaat ttagaggtta ttctcgtaaa tgatggaagt 4320

actgatgatt ctgagaaaat ttgcttaaac tatatgaaga acgatggaag aattaaatat 4380

tacaagaaaa ttaatggcgg tctagcagat gctcgaaatt tcggactaga acatgcaaca 4440

ggtaaatata ttgcttttgt cgattctgat gactatatag aagttgcaat gttcgagaga 4500

atgcatgata atataactga gtataatgcc gatatagcag agatagattt ttgtttagta 4560

gacgaaaacg ggtatacaaa gaaaaaaaga aatagtaatt ttcatgtctt aacgagagaa 4620

gagactgtaa aagaattttt gtcaggatct aatatagaaa ataatgtttg gtgcaagctt 4680

tattcacgag atattataaa agatataaaa ttccaaatta ataatagaag tattggtgag 4740

gatttgcttt ttaatttgga ggtcttgaac aatgtaacac gtgtagtagt tgatactaga 4800

gaatattatt ataattatgt cattcgtaac agttcgctta ttaatcagaa attctctata 4860

aataatattg atttagtcac aagattggag aattacccct ttaagttaaa aagagagttt 4920

agtcattatt ttgatgcaaa agttattaaa gagaaggtta aatgtttaaa caaaatgtat 4980

tcaacagatt gtttggataa tgagttcttg ccaatattag agtcttatcg aaaagaaata 5040

cgtagatatc catttattaa agcgaaaaga tatttatcaa gaaagcattt agttacgttg 5100

tatttgatga aattttcgcc taaactatat gtaatgttat ataagaaatt tcaaaagcag 5160

tagaggtaaa aatggataaa attagtgtta ttgttccagt ttataatgta gataaatatt 5220

taagtagttg tatagaaagc attattaatc aaaattataa aaatatagaa atattattga 5280

tagatgatgg ctctgtagat gattctgcta aaatatgcaa ggaatatgca gaaaaagata 5340

aaagagtaaa aatttttttc actaatcata gtggagtatc aaatgctaga aatcatggaa 5400

taaagcggag tacagctgaa tatattatgt ttgttgactc tgatgatgtt gttgatagta 5460

gattagtaga aaaattatat tttaatatta taaaaagtag aagtgattta tctggttgtt 5520

tgtacgctac tttttcagaa aatataaata attttgaagt gaataatcca aatattgatt 5580

ttgaagcaat taataccgtg caggacatgg gagaaaaaaa ttttatgaat ttgtatataa 5640

ataatatttt ttctactcct gtttgtaaac tatataagaa aagatacata acagatcttt 5700

ttcaagagaa tcaatggtta ggagaagatt tacttttttaa tctgcattat ttaaagaata 5760

tagatagagt tagttatttg actgaacatc tttatttttta taggagaggt atactaagta 5820

cagtaaattc ttttaaagaa ggtgtgtttt tgcaattgga aaatttgcaa aaacaagtga 5880

tagtattgtt taagcaaata tatggtgagg attttgacgt atcaattgtt aaagatacta 5940

tacgttggca agtattttat tatagcttac taatgtttaa atacggaaaa cagtctattt 6000

ttgacaaatt tttaattttt agaaatcttt ataaaaaata ttattttaac ttgttaaaag 6060

tatctaacaa aaattctttg tctaaaaatt tttgtataag aattgtttcg aacaaagttt 6120

ttaaaaaaat attatggtta taataggaag atatcatgga tactattagt aaaatttcta 6180

taattgtacc tatatataat gtagaaaaat atttatctaa atgtatagat agcattgtaa 6240

atcagaccta caaacatata gagattcttc tggtgaatga cggtagtacg gataattcgg 6300

aagaaatttg tttagcatat gcgaagaaag atagtcgcat tcgttatttt aaaaaagaga 6360

acggcgggct atcagatgcc cgtaattatg gcataagtcg cgccaagggt gactacttag 6420

cttttataga ctcagatgat tttattcatt cggagttcat ccaacgttta cacgaagcaa 6480

ttgagagaga gaatgccctt gtggcagttg ctggttatga tagggtagat gcttcggggc 6540

atttcttaac agcagagccg cttcctacaa atcaggctgt tctgagcggc aggaatgttt 6600

gtaaaaagct gctagaggcg gatggtcatc gctttgtggt ggcctgtaat aaactctata 6660

aaaaagaact atttgaagat tttcgatttg aaaagggtaa gattcatgaa gatgaatact 6720

tcacttatcg cttgctctat gagttagaaa aagttgcaat agttaaggag tgcttgtact 6780

attatgttga ccgagaaaat agtatcacaa cttctagcat gactgaccat cgcttccatt 6840

gcctactgga atttcaaaat gaacgaatgg acttctatga aagtagagga gataaagagc 6900

tcttactaga gtgttatcgt tcatttttag cctttgctgt tttgttttta ggcaaatata 6960

atcattggtt gagcaaacag caaaagaagc tt 6992

<210> 30

<211> 454

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS1E

<400> 30

Arg Gln Thr Lys Leu Ala Leu Phe Asp Met Ile Ala Val Ala Ile Ser
1 5 10 15

Ala Ile Leu Thr Ser His Ile Pro Asn Ala Asp Leu Asn Arg Ser Gly
20 25 30

Ile Phe Ile Ile Met Met Val His Tyr Phe Ala Phe Phe Ile Ser Arg
35 40 45

Met Pro Val Glu Phe Glu Tyr Arg Gly Asn Leu Ile Glu Phe Glu Lys
50 55 60

Thr Phe Asn Tyr Ser Ile Ile Phe Ala Ile Phe Leu Thr Ala Val Ser
65 70 75 80

Phe Leu Leu Glu Asn Asn Phe Ala Leu Ser Arg Arg Gly Ala Val Tyr
85 90 95

Phe Thr Leu Ile Asn Phe Val Leu Val Tyr Leu Phe Asn Val Ile Ile
100 105 110

Lys Gln Phe Lys Asp Ser Phe Leu Phe Ser Thr Ile Tyr Gln Lys Lys
115 120 125

Thr Ile Leu Ile Thr Thr Ala Glu Arg Trp Glu Asn Met Gln Val Leu
130 135 140

Phe Glu Ser His Lys Gln Ile Gln Lys Asn Leu Val Ala Leu Val Val
145 150 155 160

Leu Gly Thr Glu Ile Asp Lys Ile Asn Leu Ser Leu Pro Leu Tyr Tyr
165 170 175

Ser Val Glu Glu Ala Ile Glu Phe Ser Thr Arg Glu Val Val Asp His
180 185 190

Val Phe Ile Asn Leu Pro Ser Glu Phe Leu Asp Val Lys Gln Phe Val
195 200 205

Ser Asp Phe Glu Leu Leu Gly Ile Asp Val Ser Val Asp Ile Asn Ser
210 215 220

Phe Gly Phe Thr Ala Leu Lys Asn Lys Lys Ile Gln Leu Leu Gly Asp
225 230 235 240

His Ser Ile Val Thr Phe Ser Thr Asn Phe Tyr Lys Pro Ser His Ile
245 250 255

Met Met Lys Arg Leu Leu Asp Ile Leu Gly Ala Val Val Gly Leu Ile
260 265 270

Ile Cys Gly Ile Val Ser Ile Leu Leu Val Pro Ile Ile Arg Arg Asp
275 280 285

Gly Gly Pro Ala Ile Phe Ala Gln Lys Arg Val Gly Gln Asn Gly Arg
290 295 300

Ile Phe Thr Phe Tyr Lys Phe Arg Ser Met Tyr Val Asp Ala Glu Glu
305 310 315 320

Arg Lys Lys Asp Leu Leu Ser Gln Asn Gln Met Gln Gly Trp Val Cys
325 330 335

Phe Lys Met Gly Lys Thr Ile Leu Glu Leu Leu Gln Leu Asp Ile Ser
340 345 350

Tyr Ala Lys Thr Ser Leu Asp Glu Leu Pro Gln Phe Tyr Asn Val Leu
355 360 365

Ile Gly Asp Met Ser Leu Val Gly Thr Arg Pro Pro Thr Val Asp Glu
370 375 380

Phe Glu Lys Tyr Thr Pro Gly Gln Lys Arg Arg Leu Ser Phe Lys Pro
385 390 395 400

Gly Ile Thr Gly Leu Trp Gln Val Ser Gly Arg Ser Asn Ile Thr Asp
405 410 415

Phe Asp Asp Val Val Arg Leu Asp Leu Ala Tyr Ile Asp Asn Trp Thr
420 425 430

Ile Trp Ser Asp Ile Lys Ile Leu Leu Lys Thr Val Lys Val Val Leu
435 440 445

Leu Arg Glu Gly Ser Lys
450

<210> 31

<211> 149

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS1F

<400> 31

Met Lys Val Cys Leu Val Gly Ser Ser Gly Gly His Leu Thr His Leu
1 5 10 15

Tyr Leu Leu Lys Pro Phe Trp Lys Glu Glu Glu Arg Phe Trp Val Thr
20 25 30

Phe Asp Lys Glu Asp Ala Arg Ser Leu Leu Lys Asn Glu Lys Met Tyr
35 40 45

Pro Cys Tyr Phe Pro Thr Asn Arg Asn Leu Ile Asn Leu Val Lys Asn
50 55 60

Thr Phe Leu Ala Phe Lys Ile Leu Arg Asp Glu Lys Pro Asp Val Ile
65 70 75 80

Ile Ser Ser Gly Ala Ala Val Ala Val Pro Phe Phe Tyr Ile Gly Lys
85 90 95

Leu Phe Gly Ala Lys Thr Ile Tyr Ile Glu Val Phe Asp Arg Val Asn
100 105 110

Lys Ser Thr Leu Thr Gly Lys Leu Val Tyr Pro Val Thr Asp Ile Phe
115 120 125

Ile Val Gln Trp Glu Glu Met Lys Lys Val Tyr Pro Lys Ser Ile Asn
130 135 140

Leu Gly Ser Ile Phe
145

<210> 32

<211> 164

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS1G

<400> 32

Met Ile Phe Val Thr Val Gly Thr His Glu Gln Gln Phe Asn Arg Leu
1 5 10 15

Ile Lys Glu Ile Asp Leu Leu Lys Lys Asn Gly Ser Ile Thr Asp Glu
20 25 30

Ile Phe Ile Gln Thr Gly Tyr Ser Asp Tyr Ile Pro Glu Tyr Cys Lys
35 40 45

Tyr Lys Lys Phe Leu Ser Tyr Lys Glu Met Glu Gln Tyr Ile Asn Lys
50 55 60

Ser Glu Val Val Ile Cys His Gly Gly Pro Ala Thr Phe Met Asn Ser
65 70 75 80

Leu Ser Lys Gly Lys Lys Gln Leu Leu Phe Pro Arg Gln Lys Lys Tyr
85 90 95

Gly Glu His Val Asn Asp His Gln Val Glu Phe Val Arg Arg Ile Leu
100 105 110

Gln Asp Asn Asn Ile Leu Phe Ile Glu Asn Ile Asp Asp Leu Phe Glu
115 120 125

Lys Ile Ile Glu Val Ser Lys Gln Thr Asn Phe Thr Ser Asn Asn Asn
130 135 140

Phe Phe Cys Glu Arg Leu Lys Gln Ile Val Glu Lys Phe Asn Glu Asp
145 150 155 160

Gln Glu Asn Glu

<210> 33

<211> 388

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS1H

<400> 33

Met Phe Lys Leu Phe Lys Tyr Asp Pro Glu Tyr Phe Ile Phe Lys Tyr
1 5 10 15

Phe Trp Leu Ile Ile Phe Ile Pro Glu Gln Lys Tyr Val Phe Leu Leu
20 25 30

Ile Phe Met Asn Leu Ile Leu Phe His Ile Lys Phe Leu Lys Thr Lys
35 40 45

Leu Ile Leu Lys Asn Glu Ile Leu Leu Phe Leu Leu Trp Ser Ile Leu
50 55 60

Cys Phe Val Ser Val Val Thr Ser Met Phe Val Glu Ile Asn Phe Glu
65 70 75 80

Arg Leu Phe Ala Asp Phe Thr Ala Pro Ile Ile Trp Ile Ile Ala Ile
85 90 95

Met Tyr Tyr Asn Leu Tyr Ser Phe Ile Asn Ile Asp Tyr Lys Lys Leu
100 105 110

Lys Asn Ser Ile Phe Phe Ser Phe Leu Val Leu Leu Gly Ile Ser Ala
115 120 125

Leu Tyr Ile Ile Gln Asn Gly Lys Asp Ile Val Phe Leu Asp Arg His
130 135 140

Leu Ile Gly Leu Asp Tyr Leu Ile Thr Gly Val Lys Thr Arg Leu Val
145 150 155 160

Gly Phe Met Asn Tyr Pro Thr Leu Asn Thr Thr Thr Ile Ile Val Ser
165 170 175

Ile Pro Leu Ile Phe Ala Leu Ile Lys Asn Lys Met Gln Gln Phe Phe
180 185 190

Phe Leu Cys Leu Ala Phe Ile Pro Ile Tyr Leu Ser Gly Ser Arg Ile
195 200 205

Gly Ser Leu Ser Leu Ala Ile Leu Ile Ile Cys Leu Leu Trp Arg Tyr
210 215 220

Ile Gly Gly Lys Phe Ala Trp Ile Lys Lys Leu Ile Val Ile Phe Val
225 230 235 240

Ile Leu Leu Ile Ile Leu Asn Thr Glu Leu Leu Tyr His Glu Ile Leu
245 250 255

Ala Val Tyr Asn Ser Arg Glu Ser Ser Asn Glu Ala Arg Phe Ile Ile
260 265 270

Tyr Gln Gly Ser Ile Asp Lys Val Leu Glu Asn Asn Ile Leu Phe Gly
275 280 285

Tyr Gly Ile Ser Glu Tyr Ser Val Thr Gly Thr Trp Leu Gly Ser His
290 295 300

Ser Gly Tyr Ile Ser Phe Phe Tyr Lys Ser Gly Ile Val Gly Leu Ile
305 310 315 320

Leu Leu Met Phe Ser Phe Phe Tyr Val Ile Lys Lys Ser Tyr Gly Val
325 330 335

Asn Gly Glu Thr Ala Leu Phe Tyr Phe Thr Ser Leu Ala Ile Phe Phe
340 345 350

Ile Tyr Glu Thr Ile Asp Pro Ile Ile Ile Ile Leu Val Leu Phe Phe
355 360 365

Ser Ser Ile Gly Ile Trp Asn Asn Ile Asn Phe Lys Lys Asp Met Glu
370 375 380

Thr Lys Asn Glu
385

<210> 34

<211> 322

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS1I

<400> 34

Met Asn Asp Leu Ile Ser Val Ile Val Pro Ile Tyr Asn Val Gln Asp
1 5 10 15

Tyr Leu Asp Lys Cys Ile Asn Ser Ile Ile Asn Gln Thr Tyr Thr Asn
20 25 30

Leu Glu Val Ile Leu Val Asn Asp Gly Ser Thr Asp Asp Ser Glu Lys
35 40 45

Ile Cys Leu Asn Tyr Met Lys Asn Asp Gly Arg Ile Lys Tyr Tyr Lys
50 55 60

Lys Ile Asn Gly Gly Leu Ala Asp Ala Arg Asn Phe Gly Leu Glu His
65 70 75 80

Ala Thr Gly Lys Tyr Ile Ala Phe Val Asp Ser Asp Asp Tyr Ile Glu
85 90 95

Val Ala Met Phe Glu Arg Met His Asp Asn Ile Thr Glu Tyr Asn Ala
100 105 110

Asp Ile Ala Glu Ile Asp Phe Cys Leu Val Asp Glu Asn Gly Tyr Thr
115 120 125

Lys Lys Lys Arg Asn Ser Asn Phe His Val Leu Thr Arg Glu Glu Thr
130 135 140

Val Lys Glu Phe Leu Ser Gly Ser Asn Ile Glu Asn Asn Val Trp Cys
145 150 155 160

Lys Leu Tyr Ser Arg Asp Ile Ile Lys Asp Ile Lys Phe Gln Ile Asn
165 170 175

Asn Arg Ser Ile Gly Glu Asp Leu Leu Phe Asn Leu Glu Val Leu Asn
180 185 190

Asn Val Thr Arg Val Val Val Asp Thr Arg Glu Tyr Tyr Tyr Asn Tyr
195 200 205

Val Ile Arg Asn Ser Ser Leu Ile Asn Gln Lys Phe Ser Ile Asn Asn
210 215 220

Ile Asp Leu Val Thr Arg Leu Glu Asn Tyr Pro Phe Lys Leu Lys Arg
225 230 235 240

Glu Phe Ser His Tyr Phe Asp Ala Lys Val Ile Lys Glu Lys Val Lys
245 250 255

Cys Leu Asn Lys Met Tyr Ser Thr Asp Cys Leu Asp Asn Glu Phe Leu
260 265 270

Pro Ile Leu Glu Ser Tyr Arg Lys Glu Ile Arg Arg Tyr Pro Phe Ile
275 280 285

Lys Ala Lys Arg Tyr Leu Ser Arg Lys His Leu Val Thr Leu Tyr Leu
290 295 300

Met Lys Phe Ser Pro Lys Leu Tyr Val Met Leu Tyr Lys Lys Phe Gln
305 310 315 320

Lys Gln

<210> 35

<211> 322

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS1J

<400> 35

Met Asp Lys Ile Ser Val Ile Val Pro Val Tyr Asn Val Asp Lys Tyr
1 5 10 15

Leu Ser Ser Cys Ile Glu Ser Ile Ile Asn Gln Asn Tyr Lys Asn Ile
20 25 30

Glu Ile Leu Leu Ile Asp Asp Gly Ser Val Asp Asp Ser Ala Lys Ile
35 40 45

Cys Lys Glu Tyr Glu Lys Asp Lys Arg Val Lys Ile Phe Phe Thr Asn
50 55 60

His Ser Gly Val Ser Asn Ala Arg Asn His Gly Ile Lys Arg Ser Thr
65 70 75 80

Ala Glu Tyr Ile Met Phe Val Asp Ser Asp Asp Val Val Asp Ser Arg
85 90 95

Leu Val Glu Lys Leu Tyr Phe Asn Ile Ile Lys Ser Arg Ser Asp Leu
100 105 110

Ser Gly Cys Leu Tyr Ala Thr Phe Ser Glu Asn Ile Asn Asn Phe Glu
115 120 125

Val Asn Asn Pro Asn Ile Asp Phe Glu Ala Ile Asn Thr Val Gln Asp
130 135 140

Met Gly Glu Lys Asn Phe Met Asn Leu Tyr Ile Asn Asn Ile Phe Ser
145 150 155 160

Thr Pro Val Cys Lys Leu Tyr Lys Lys Arg Tyr Ile Thr Asp Leu Phe
165 170 175

Gln Glu Asn Gln Trp Leu Gly Glu Asp Leu Leu Phe Asn Leu His Tyr
180 185 190

Leu Lys Asn Ile Asp Arg Val Ser Tyr Leu Thr Glu His Leu Tyr Phe
195 200 205

Tyr Arg Arg Gly Ile Leu Ser Thr Val Asn Ser Phe Lys Glu Gly Val
210 215 220

Phe Leu Gln Leu Glu Asn Leu Gln Lys Gln Val Ile Val Leu Phe Lys
225 230 235 240

Gln Ile Tyr Gly Glu Asp Phe Asp Val Ser Ile Val Lys Asp Thr Ile
245 250 255

Arg Trp Gln Val Phe Tyr Tyr Ser Leu Leu Met Phe Lys Tyr Gly Lys
260 265 270

Gln Ser Ile Phe Asp Lys Phe Leu Ile Phe Arg Asn Leu Tyr Lys Lys
275 280 285

Tyr Tyr Phe Asn Leu Leu Lys Val Ser Asn Lys Asn Ser Leu Ser Lys
290 295 300

Asn Phe Cys Ile Arg Ile Val Ser Asn Lys Val Phe Lys Lys Ile Leu
305 310 315 320

Trp Leu

<210> 36

<211> 278

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS1K

<400> 36

Met Asp Thr Ile Ser Lys Ile Ser Ile Ile Val Pro Ile Tyr Asn Val
1 5 10 15

Glu Lys Tyr Leu Ser Lys Cys Ile Asp Ser Ile Val Asn Gln Thr Tyr
20 25 30

Lys His Ile Glu Ile Leu Leu Val Asn Asp Gly Ser Thr Asp Asn Ser
35 40 45

Glu Glu Ile Cys Leu Ala Tyr Ala Lys Lys Asp Ser Arg Ile Arg Tyr
50 55 60

Phe Lys Lys Glu Asn Gly Gly Leu Ser Asp Ala Arg Asn Tyr Gly Ile
65 70 75 80

Ser Arg Ala Lys Gly Asp Tyr Leu Ala Phe Ile Asp Ser Asp Asp Phe
85 90 95

Ile His Ser Glu Phe Ile Gln Arg Leu His Glu Ala Ile Glu Arg Glu
100 105 110

Asn Ala Leu Val Ala Val Ala Gly Tyr Asp Arg Val Asp Ala Ser Gly
115 120 125

His Phe Leu Thr Ala Glu Pro Leu Pro Thr Asn Gln Ala Val Leu Ser
130 135 140

Gly Arg Asn Val Cys Lys Lys Leu Leu Glu Ala Asp Gly His Arg Phe
145 150 155 160

Val Val Ala Cys Asn Lys Leu Tyr Lys Lys Glu Leu Phe Glu Asp Phe
165 170 175

Arg Phe Glu Lys Gly Lys Ile His Glu Asp Glu Tyr Phe Thr Tyr Arg
180 185 190

Leu Leu Tyr Glu Leu Glu Lys Val Ala Ile Val Lys Glu Cys Leu Tyr
195 200 205

Tyr Tyr Val Asp Arg Glu Asn Ser Ile Thr Thr Ser Ser Met Thr Asp
210 215 220

His Arg Phe His Cys Leu Leu Glu Phe Gln Asn Glu Arg Met Asp Phe
225 230 235 240

Tyr Glu Ser Arg Gly Asp Lys Glu Leu Leu Leu Glu Cys Tyr Arg Ser
245 250 255

Phe Leu Ala Phe Ala Val Leu Phe Leu Gly Lys Tyr Asn His Trp Leu
260 265 270

Ser Lys Gln Gln Lys Lys
275

<210> 37

<211> 4519

<212> DNA

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS9

<400> 37

aagcttatcg tcaaggtgtt cgctatatcg tggcgacatc tcatagacga aaagggatgt 60

ttgaaacacc agaaaaagtt atcatgacta actttcttca atttaaagac gcagtagcag 120

aagtttatcc tgaaatacga ttgtgctatg gtgctgaatt gtattatagt aaagatatat 180

taagcaaact tgaaaaaaag aaagtaccca cacttaatgg ctcgcgctat attcttttgg 240

agttcagtag tgatactcct tggaaagaga ttcaagaagc agtgaacgaa gtgacgctac 300

ttgggctaac tcccgtactt gcccatatag aacgatatga cgccctagcg tttcatgcag 360

agagagtaga agagttaatt gacaagggat gctatactca ggtaaatagt aatcatgtgc 420

tgaagcccac tttaattggt gatcgagcaa aagaatttaa aaaacgtact cggtattttt 480

tagagcagga tttagtacat tgtgttgcta gcgatatgca taatttatct agtagacctc 540

cgtttatgag ggaggcttat aagttgctaa cagaggaatt tggcaaagat aaagcgaaag 600

cgttgctaaa aaagaatcct cttatgctat taaaaaacca ggcgatttaa actggttact 660

ctagattgtg gagagaaaaa tggatttagg aactgttact gataaactgt tagaacgcaa 720

cagtaaacga ttgatactcg tgtgcatgga tacgtgtctt cttatagttt ccatgatttt 780

gagcagactg tttttggatg ttattattga cataccagat gaacgcttca ttcttgcagt 840

tttattcgta tcaattttat atttgattct atcgtttaga ttaaaagtct tttcattaat 900

tacgcgttac acagggtatc agagttatgt aaaaatagga cttagtttaa tatctgcgca 960

ttcattgttt ttaattatct caatggtgtt gtggcaggct tttagttatc gtttcatctt 1020

agtatcctta tttttgtcgt atgtaatgct cattactccg aggattgttt ggaaagtctt 1080

acatgagacg agaaaaaatg ctatccgtaa gaaggatagc ccactaagaa tcttagtagt 1140

aggtgctgga gatggtggta atatttttat caatactgtc aaagatcgaa aattgaattt 1200

tgaaattgtc ggtatcgttg atcgtgatcc aaataaactt ggaacattta tccgtacggc 1260

taaagtttta ggaaaccgta atgatattcc acgactggta gaggaattag ctgttgacca 1320

agtgacgatt gccatccctt ctttaaatgg taaggagcga gagaagattg ttgaaatctg 1380

taacactaca ggagtgaccg tcaataatat gccgagtatt gaagacatta tggcggggaa 1440

catgtctgtc agtgcctttc aggaaattga cgtagcagac cttcttggtc gaccagaggt 1500

tgttttggat caggatgaat tgaatcagtt tttccaaggg aaaacaatcc ttgtcacagg 1560

agcaggtggc tctatcggtt cagagctatg tcgtcaaatt gctaagttta cgcctaaacg 1620

cttgttgttg cttggacatg gagaaaattc aatctatctc attcatcgag agttactgga 1680

aaagtaccaa ggtaagattg agttggtccc tctcattgca gatattcaag atagagaatt 1740

gatttttagc ataatggctg aatatcaacc cgatgttgtt tatcatgctg cagcacataa 1800

gcatgttcct ttgatggaat ataatccaca tgaagcagtg aagaataata tttttggaac 1860

gaagaatgtg gctgaggcgg ctaaaactgc aaaggttgcc aaatttgtta tggtttcaac 1920

agataaagct gttaatccac caaatgtcat gggagcgact aaacgtgttg cagaaatgat 1980

tgttacaggt ttaaacgagc caggtcagac tcaatttgcg gcagtccggt ttgggaatgt 2040

tctaggtagt cgtggaagtg ttgttccgct attcaaagag caaattagaa aaggtggacc 2100

tgttacggtt accgacttta ggatgactcg ttatttcatg acgattcctg aggcaagtcg 2160

tttggttatc caagctggac atttggcaaa aggtggagaa atatttgtct tggatatggg 2220

cgagccagta caaatcctgg aattggcaag aaaagttatc ttgttaagtg gacacacaga 2280

ggaagaaatc gggattgtag aatctggaat cagaccaggc gagaaactct acgaggaatt 2340

attatcaaca gaagaacgtg tcagcgaaca gattcatgaa aaaatatttg tgggtcgcgt 2400

tacaaataag cagtcggaca ttgtcaattc atttatcaat ggattactcc aaaaagatag 2460

aaatgaatta aaaaatatgt tgattgaatt tgcaaaacaa gaataagaaa gtaaaaaata 2520

tttttacttt cctagagttt aaacgatgtt taagttctag gaaggttaga atacctaatt 2580

aacaacaata ttactattta ttaagagtca gataatagca actaagtgct acaaactatc 2640

tttataataa gtatatttgg tcaaaaggga gatgtgaaat gtatccaatt tgtaaacgta 2700

ttttagcaat tattatctca gggattgcta ttgttgttct gagtccaatt ttattattga 2760

ttgcattggc aattaaatta gattctaaag gtccggtatt atttaaacaa aagcgggttg 2820

gtaaaaacaa gtcatacttt atgatttata aattccgttc tatgtacgtt gacgcaccaa 2880

gtgatatgcc gactcatcta ttaaaggatc ctaaggcgat gattaccaag gtgggcgcgt 2940

ttctcagaaa aacaagttta gatgaactgc cacagctttt taatattttt aaaggtgaaa 3000

tggcgattgt tggtccacgc ccagccttat ggaatcaata tgacttaatt gaagagcgag 3060

ataaatatgg tgcaaatgat attcgtcctg gactaaccgg ttgggctcaa attaatggtc 3120

gtgatgaatt ggaaattgat gaaaagtcaa aattagatgg atattatgtt caaaatatga 3180

gtctaggttt ggatattaaa tgtttcttag gtacattcct cagtgtagcc agaagcgaag 3240

gtgttgttga aggtggaaca gggcagaaag gaaaaggatg aaattttcag tattaatgtc 3300

ggtctatgag aaagaaaaac cagagtttct tagggaatct ttggaaagca tccttgtcaa 3360

tcaaacaatg attccaacgg aggttgtctt ggtagaggat gggccactca atcagagctt 3420

atatagtatt ttagaagaat ttaaaagtcg attttcattt tttaaaacga tagccttgga 3480

aaagaattcg ggtttaggaa ttgcactgaa tgaaggtttg aaacattgta attatgagtg 3540

ggtttgcacg aaatggattc tgatgatgtt gcatatacat acacgttttg aaaagcaagt 3600

taactttata aaacaaaacc cgactataga tattgagata gatgagttct taaattctac 3660

tagtgaaata gtttctcata aaaatgttcc aacccagcac gatgaaatat taaagatggc 3720

aaggcgggag aaatccatgt gccacatgac tgtaatgttt aaaaagaaaa gtgtcgagag 3780

agcagggggg tatcaaacac ttccgtacgt agaagattat ttcctttggg tgcgcatgat 3840

tgcttcagga tcgaaatttg caaacattga tgaaacacta gttcttgcac gtgttggaaa 3900

tgggatgttc aataggaggg ggaacagaga acaaattaac agttggacat tactaattga 3960

atttatgtta gctcaaggaa ttgttacacc actagatgta tttattaatc aaatttacat 4020

tagggtcttt gtttatatgc caacttggat aaagaaactc atttatggaa aaatcttaag 4080

gaaatagtat gattacagta ttgatggcta catataatgg aagcccattt ataataaaac 4140

agttagattc aattcgaaat caaagtgtat cagcagacaa agttattatt tgggatgatt 4200

gctcgacaga tgatacaata aaaataataa aagattatat aaaaaaatat tctttggatt 4260

catgggttgt ctctcaaaat aaatctaatc aggggcatta tcaaacattt ataaatttga 4320

caaagttagt tcaggaagga atagtctttt tttcagatca agatgatatt tgggactgtc 4380

ataaaattga gacaatgctt ccaatctttg acagagaaaa tgtatcaatg gtgttttgca 4440

aatccagatt gattgatgaa aacggaaata ttatcagtag cccagatact tcggatagaa 4500

tcaatacgta ctctctaga 4519

<210> 38

<211> 215

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS9D

<400> 38

Ala Tyr Arg Gln Gly Val Arg Tyr Ile Val Ala Thr Ser His Arg Arg
1 5 10 15

Lys Gly Met Phe Glu Thr Pro Glu Lys Val Ile Met Thr Asn Phe Leu
20 25 30

Gln Phe Lys Asp Ala Val Ala Glu Val Tyr Pro Glu Ile Arg Leu Cys
35 40 45

Tyr Gly Ala Glu Leu Tyr Tyr Ser Lys Asp Ile Leu Ser Lys Leu Glu
50 55 60

Lys Lys Lys Val Pro Thr Leu Asn Gly Ser Arg Tyr Ile Leu Leu Glu
65 70 75 80

Phe Ser Ser Asp Thr Pro Trp Lys Glu Ile Gln Glu Ala Val Asn Glu
85 90 95

Val Thr Leu Leu Gly Leu Thr Pro Val Leu Ala His Ile Glu Arg Tyr
100 105 110

Asp Ala Leu Ala Phe His Ala Glu Arg Val Glu Glu Leu Ile Asp Lys
115 120 125

Gly Cys Tyr Thr Gln Val Asn Ser Asn His Val Leu Lys Pro Thr Leu
130 135 140

Ile Gly Asp Arg Ala Lys Glu Phe Lys Lys Arg Thr Arg Tyr Phe Leu
145 150 155 160

Glu Gln Asp Leu Val His Cys Val Ala Ser Asp Met His Asn Leu Ser
165 170 175

Ser Arg Pro Pro Phe Met Arg Glu Ala Tyr Lys Leu Leu Thr Glu Glu
180 185 190

Phe Gly Lys Asp Lys Ala Lys Ala Leu Leu Lys Lys Asn Pro Leu Met
195 200 205

Leu Leu Lys Asn Gln Ala Ile
210 215

<210> 39

<211> 608

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS9E

<400> 39

Met Asp Leu Gly Thr Val Thr Asp Lys Leu Leu Glu Arg Asn Ser Lys
1 5 10 15

Arg Leu Ile Leu Val Cys Met Asp Thr Cys Leu Leu Ile Val Ser Met
20 25 30

Ile Leu Ser Arg Leu Phe Leu Asp Val Ile Ile Asp Ile Pro Asp Glu
35 40 45

Arg Phe Ile Leu Ala Val Leu Phe Val Ser Ile Leu Tyr Leu Ile Leu
50 55 60

Ser Phe Arg Leu Lys Val Phe Ser Leu Ile Thr Arg Tyr Thr Gly Tyr
65 70 75 80

Gln Ser Tyr Val Lys Ile Gly Leu Ser Leu Ile Ser Ala His Ser Leu
85 90 95

Phe Leu Ile Ile Ser Met Val Leu Trp Gln Ala Phe Ser Tyr Arg Phe
100 105 110

Ile Leu Val Ser Leu Phe Leu Ser Tyr Val Met Leu Ile Thr Pro Arg
115 120 125

Ile Val Trp Lys Val Leu His Glu Thr Arg Lys Asn Ala Ile Arg Lys
130 135 140

Lys Asp Ser Pro Leu Arg Ile Leu Val Val Gly Ala Gly Asp Gly Gly
145 150 155 160

Asn Ile Phe Ile Asn Thr Val Lys Asp Arg Lys Leu Asn Phe Glu Ile
165 170 175

Val Gly Ile Val Asp Arg Asp Pro Asn Lys Leu Gly Thr Phe Ile Arg
180 185 190

Thr Ala Lys Val Leu Gly Asn Arg Asn Asp Ile Pro Arg Leu Val Glu
195 200 205

Glu Leu Ala Val Asp Gln Val Thr Ile Ala Ile Pro Ser Leu Asn Gly
210 215 220

Lys Glu Arg Glu Lys Ile Val Glu Ile Cys Asn Thr Thr Gly Val Thr
225 230 235 240

Val Asn Asn Met Pro Ser Ile Glu Asp Ile Met Ala Gly Asn Met Ser
245 250 255

Val Ser Ala Phe Gln Glu Ile Asp Val Ala Asp Leu Leu Gly Arg Pro
260 265 270

Glu Val Val Leu Asp Gln Asp Glu Leu Asn Gln Phe Phe Gln Gly Lys
275 280 285

Thr Ile Leu Val Thr Gly Ala Gly Gly Ser Ile Gly Ser Glu Leu Cys
290 295 300

Arg Gln Ile Ala Lys Phe Thr Pro Lys Arg Leu Leu Leu Leu Gly His
305 310 315 320

Gly Glu Asn Ser Ile Tyr Leu Ile His Arg Glu Leu Leu Glu Lys Tyr
325 330 335

Gln Gly Lys Ile Glu Leu Val Pro Leu Ile Ala Asp Ile Gln Asp Arg
340 345 350

Glu Leu Ile Phe Ser Ile Met Ala Glu Tyr Gln Pro Asp Val Val Tyr
355 360 365

His Ala Ala Ala His Lys His Val Pro Leu Met Glu Tyr Asn Pro His
370 375 380

Glu Ala Val Lys Asn Asn Ile Phe Gly Thr Lys Asn Val Ala Glu Ala
385 390 395 400

Ala Lys Thr Ala Lys Val Ala Lys Phe Val Met Val Ser Thr Asp Lys
405 410 415

Ala Val Asn Pro Pro Asn Val Met Gly Ala Thr Lys Arg Val Ala Glu
420 425 430

Met Ile Val Thr Gly Leu Asn Glu Pro Gly Gln Thr Gln Phe Ala Ala
435 440 445

Val Arg Phe Gly Asn Val Leu Gly Ser Arg Gly Ser Val Val Pro Leu
450 455 460

Phe Lys Glu Gln Ile Arg Lys Gly Gly Pro Val Thr Val Thr Asp Phe
465 470 475 480

Arg Met Thr Arg Tyr Phe Met Thr Ile Pro Glu Ala Ser Arg Leu Val
485 490 495

Ile Gln Ala Gly His Leu Ala Lys Gly Gly Glu Ile Phe Val Leu Asp
500 505 510

Met Gly Glu Pro Val Gln Ile Leu Glu Leu Ala Arg Lys Val Ile Leu
515 520 525

Leu Ser Gly His Thr Glu Glu Glu Ile Gly Ile Val Glu Ser Gly Ile
530 535 540

Arg Pro Gly Glu Lys Leu Tyr Glu Glu Leu Leu Ser Thr Glu Glu Arg
545 550 555 560

Val Ser Glu Gln Ile His Glu Lys Ile Phe Val Gly Arg Val Thr Asn
565 570 575

Lys Gln Ser Asp Ile Val Asn Ser Phe Ile Asn Gly Leu Leu Gln Lys
580 585 590

Asp Arg Asn Glu Leu Lys Asn Met Leu Ile Glu Phe Ala Lys Gln Glu
595 600 605

<210> 40

<211> 200

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS9F

<400> 40

Met Tyr Pro Ile Cys Lys Arg Ile Leu Ala Ile Ile Ile Ser Gly Ile
1 5 10 15

Ala Ile Val Val Leu Ser Pro Ile Leu Leu Leu Ile Ala Leu Ala Ile
20 25 30

Lys Leu Asp Ser Lys Gly Pro Val Leu Phe Lys Gln Lys Arg Val Gly
35 40 45

Lys Asn Lys Ser Tyr Phe Met Ile Tyr Lys Phe Arg Ser Met Tyr Val
50 55 60

Asp Ala Pro Ser Asp Met Pro Thr His Leu Leu Lys Asp Pro Lys Ala
65 70 75 80

Met Ile Thr Lys Val Gly Ala Phe Leu Arg Lys Thr Ser Leu Asp Glu
85 90 95

Leu Pro Gln Leu Phe Asn Ile Phe Lys Gly Glu Met Ala Ile Val Gly
100 105 110

Pro Arg Pro Ala Leu Trp Asn Gln Tyr Asp Leu Ile Glu Glu Arg Asp
115 120 125

Lys Tyr Gly Ala Asn Asp Ile Arg Pro Gly Leu Thr Gly Trp Ala Gln
130 135 140

Ile Asn Gly Arg Asp Glu Leu Glu Ile Asp Glu Lys Ser Lys Leu Asp
145 150 155 160

Gly Tyr Tyr Val Gln Asn Met Ser Leu Gly Leu Asp Ile Lys Cys Phe
165 170 175

Leu Gly Thr Phe Leu Ser Val Ala Arg Ser Glu Gly Val Val Glu Gly
180 185 190

Gly Thr Gly Gln Lys Gly Lys Gly
195 200

<210> 41

<211> 269

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS2G

<400> 41

Met Lys Phe Ser Val Leu Met Ser Val Tyr Glu Lys Glu Lys Pro Glu
1 5 10 15

Phe Leu Arg Glu Ser Leu Glu Ser Ile Leu Val Asn Gln Thr Met Ile
20 25 30

Pro Thr Glu Val Val Leu Val Glu Asp Gly Pro Leu Asn Gln Ser Leu
35 40 45

Tyr Ser Ile Leu Glu Glu Phe Lys Ser Arg Phe Ser Phe Phe Lys Thr
50 55 60

Ile Ala Leu Glu Lys Asn Ser Gly Leu Gly Ile Ala Leu Asn Glu Gly
65 70 75 80

Leu Lys His Cys Asn Tyr Glu Trp Val Cys Thr Lys Trp Ile Leu Met
85 90 95

Met Leu His Ile His Thr Arg Phe Glu Lys Gln Val Asn Phe Ile Lys
100 105 110

Gln Asn Pro Thr Ile Asp Ile Glu Ile Asp Glu Phe Leu Asn Ser Thr
115 120 125

Ser Glu Ile Val Ser His Lys Asn Val Pro Thr Gln His Asp Glu Ile
130 135 140

Leu Lys Met Ala Arg Arg Glu Lys Ser Met Cys His Met Thr Val Met
145 150 155 160

Phe Lys Lys Lys Ser Val Glu Arg Ala Gly Gly Tyr Gln Thr Leu Pro
165 170 175

Tyr Val Glu Asp Tyr Phe Leu Trp Val Arg Met Ile Ala Ser Gly Ser
180 185 190

Lys Phe Ala Asn Ile Asp Glu Thr Leu Val Leu Ala Arg Val Gly Asn
195 200 205

Gly Met Phe Asn Arg Arg Gly Asn Arg Glu Gln Ile Asn Ser Trp Thr
210 215 220

Leu Leu Ile Glu Phe Met Leu Ala Gln Gly Ile Val Thr Pro Leu Asp
225 230 235 240

Val Phe Ile Asn Gln Ile Tyr Ile Arg Val Phe Val Tyr Met Pro Thr
245 250 255

Trp Ile Lys Lys Leu Ile Tyr Gly Lys Ile Leu Arg Lys
260 265

<210> 42

<211> 143

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS9H

<400> 42

Met Ile Thr Val Leu Met Ala Thr Tyr Asn Gly Ser Pro Phe Ile Ile
1 5 10 15

Lys Gln Leu Asp Ser Ile Arg Asn Gln Ser Val Ser Ala Asp Lys Val
20 25 30

Ile Ile Trp Asp Asp Cys Ser Thr Asp Asp Thr Ile Lys Ile Ile Lys
35 40 45

Asp Tyr Ile Lys Lys Tyr Ser Leu Asp Ser Trp Val Val Ser Gln Asn
50 55 60

Lys Ser Asn Gln Gly His Tyr Gln Thr Phe Ile Asn Leu Thr Lys Leu
65 70 75 80

Val Gln Glu Gly Ile Val Phe Phe Ser Asp Gln Asp Asp Ile Trp Asp
85 90 95

Cys His Lys Ile Glu Thr Met Leu Pro Ile Phe Asp Arg Glu Asn Val
100 105 110

Ser Met Val Phe Cys Lys Ser Arg Leu Ile Asp Glu Asn Gly Asn Ile
115 120 125

Ile Ser Ser Pro Asp Thr Ser Asp Arg Ile Asn Thr Tyr Ser Leu
130 135 140

<210> 43

<211> 3738

<212> DNA

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS7

<400> 43

ctgcagcaca taagcatgtt ccattgatgg aatataatcc acatgaagca gtgaagaata 60

atatttttgg aacgaagaat gtggctgagg cggctaaaac tgcaaaggtt gccaaatttg 120

ttatggtttc aacagataaa gctgttaatc cgccaaatgt catgggagcg actaaacgtg 180

ttgcagaaat gattgtaaca ggtttaaacg agccaggtca gactcaattt gcggcagtcc 240

gttttgggaa tgttctaggt agtcgtggaa gtgttgttcc gctattcaaa gagcaaatta 300

gaaaaggtgg acctgttacg gttaccgact ttaggatgac tcgttatttc atgacgattc 360

ctgaggcaag tcgtttggtt atccaagctg gacatttggc aaaaggtgga gaaatctttg 420

tcttggatat gggtgagcca gtacaaatcc tggaattggc aagaaaagtt atcttgttaa 480

gcggacatac agaggaagaa atcgggattg tagaatctgg aatcagacca ggcgagaaac 540

tctacgagga attgttatca acagaagaac gtgtcagcga acagattcat gaaaaaatat 600

ttgtgggtcg cgttacaaat aagcagtcgg acattgtcaa ttcatttatc aatggattac 660

tccaaaaaga tagaaatgaa ttaaaagata tgttgattga atttgcaaaa caagaataag 720

aaagtaaaaa atatttttac tttcctagag tttaaacgat gtttaagttc taggaaggtt 780

ggaattgctt tcgtggaggt gatagataga aacctatata tttgtagaag aaaggatatt 840

aaactaaagg tgaatcggaa cataaagttt agatagagtt ggtatttaat gccaaacagg 900

tgaatgcaac ctctcgctcg ttactaagca ggagatagta aagttgcttg aaagagagtt 960

tgttaatcag tataagtagg ctaaagtgag aatatatatc tattattatc ggtaatgata 1020

ctattattga gaattattgt agtggggata aaaataattt ttggtgattt tatcgtccga 1080

cttaaaggtg ggttaaaaaa gtacttatat tcttttagaa ttgatgaaaa atatgggggga 1140

atataatatt tataggagat acgatgacta gagtagagtt gattactaga gaatttttta 1200

agaagaatga agcaaccagt aaatattttc agaagataga atcaagaaga ggtgaattat 1260

ttattaaatt ctttatggat aagttacttg cgcttatcct attattgcta ttatccccag 1320

taatcattat attagctatt tggataaaat tagatagtaa ggggccaatt ttttatcgcc 1380

aagaacgtgt tacgagatat ggtcgaattt ttagaatatt taagtttaga acaatgattt 1440

ctgatgcgga taaagtcgga agtcttgtca cagtcggtca agataatcgt attacgaaag 1500

tcggtcacat tatcagaaaa tatcggctgg acgaagtgcc ccaacttttt aatgttttaa 1560

tgggggatat gagctttgta ggtgtaagac cagaagtaca aaaatatgta aatcagtata 1620

ctgatgaaat gtttgcgacg ttacttttac ctgcaggaat tacttcacca gcgagtattg 1680

catataagga tgaagatatt gttttagaag aatattgttc tcaaggctat agtcctgatg 1740

aagcatatgt tcaaaaagta ttaccagaaa aaatgaagta caatttggaa tatatcagaa 1800

actttggaat tatttctgat tttaaagtaa tgattgatac agtaattaaa gtaataaaat 1860

aggagattaa aatgacaaaa agacaaaata ttccattttc accaccagat attacccaag 1920

ctgaaattga tgaagttatt gacacactaa aatctggttg gattacaaca ggaccaaaga 1980

caaaagagct agaacgtcgg ctatcagtat ttacaggaac caataaaact gtgtgtttaa 2040

attctgctac tgcaggattg gaactagtct tacgaattct tggtgttgga cccggagatg 2100

aagttattgt tcctgctatg acctatactg cctcatgtag tgtcattact catgtaggag 2160

caactcctgt gatggttgat attcaaaaaa acagctttga gatggaatat gatgctttgg 2220

aaaaagcgat tactccgaaa acaaaagtta tcattcctgt tgatctagct ggtattcctt 2280

gtgattatga taagatttat accatcgtag aaaacaaacg ctctttgtat gttgcttctg 2340

ataataaatg gcagaaactt tttgggcgag ttattatcct atctgatagt gcacactcac 2400

taggtgctag ttataaggga aaaccagcgg gttccctagc agattttacc tcattttctt 2460

tccatgcagt taagaatttt acaactgctg aaggaggtag tgtgacatgg agatcacatc 2520

ctgatttgga tgacgaagag atgtataaag agtttcagat ttactctctt catggtcaga 2580

caaaggatgc attagctaag acacaattag ggtcatggga atatgacatt gttattcctg 2640

gttacaagtg taatatgaca gatattatgg caggtatcgg tcttgtgcaa ttagaacgtt 2700

acccatcttt gttgaatcgt cgcagagaaa tcattgagaa atacaatgct ggctttgagg 2760

ggacttcgat taagccgttg gtacacctga cggaagataa acaatcgtct atgcacttgt 2820

atatcacgca tctacaaggc tatactttag aacaacgaaa tgaagtcatt caaaaaatgg 2880

ctgaagcagg tattgcgtgc aatgttcact acaaaccatt acctcttctc acagcctaca 2940

agaatcttgg ttttgaaatg aaagattttc cgaatgccta tcagtatttt gaaaatgaag 3000

ttacactgcc tcttcatacc aacttgagtg atgaagatgt ggagtatgtg atagaaatgt 3060

ttttaaaaat tgttagtaga gattagttat tttggaagga gatatggtgg aaagagatat 3120

ggtggaaaga gacacgttgg tatctataat aatgccctcg tggaatacag ctaagtatat 3180

atctgaatca atccagtcag tgttggacca aacacaccaa aattgggaac ttataatcgt 3240

tgatgattgt tctaatgacg aaactgaaaa agttgtttcg catttcaaag attcaagaat 3300

aaagtttttt aaaaattcga ataatttagg ggcagctcta acacgaaata aggcactaag 3360

aaaagctaga ggtaggtgga ttgcgttctt ggattcagat gatttatggc acccgagtaa 3420

gctagaaaaa cagcttgaat ttatgaaaaa taatggatat tcatttactt atcacaattt 3480

tgaaaagatt gatgaatcta gtcagtcttt acgtgtcctg gtgtcaggac cagcaattgt 3540

gactagaaaa atgatgtaca attacggcta tccagggtgt ttgactttca tgtatgatgc 3600

agacaaaatg ggtttaattc agataaaaga tataaagaaa aataacgatt atgcgatatt 3660

acttcaattg tgtaagaagt atgactgtta tcttttaaat gaaagtttag cttcgtatcg 3720

aattagaaaa aaatcgat 3738

<210> 44

<211> 238

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS7E

<400> 44

Ala Ala His Lys His Val Pro Leu Met Glu Tyr Asn Pro His Glu Ala
1 5 10 15

Val Lys Asn Asn Ile Phe Gly Thr Lys Asn Val Ala Glu Ala Ala Lys
20 25 30

Thr Ala Lys Val Ala Lys Phe Val Met Val Ser Thr Asp Lys Ala Val
35 40 45

Asn Pro Pro Asn Val Met Gly Ala Thr Lys Arg Val Ala Glu Met Ile
50 55 60

Val Thr Gly Leu Asn Glu Pro Gly Gln Thr Gln Phe Ala Ala Val Arg
65 70 75 80

Phe Gly Asn Val Leu Gly Ser Arg Gly Ser Val Val Pro Leu Phe Lys
85 90 95

Glu Gln Ile Arg Lys Gly Gly Pro Val Thr Val Thr Asp Phe Arg Met
100 105 110

Thr Arg Tyr Phe Met Thr Ile Pro Glu Ala Ser Arg Leu Val Ile Gln
115 120 125

Ala Gly His Leu Ala Lys Gly Gly Glu Ile Phe Val Leu Asp Met Gly
130 135 140

Glu Pro Val Gln Ile Leu Glu Leu Ala Arg Lys Val Ile Leu Leu Ser
145 150 155 160

Gly His Thr Glu Glu Glu Ile Gly Ile Val Glu Ser Gly Ile Arg Pro
165 170 175

Gly Glu Lys Leu Tyr Glu Glu Leu Leu Ser Thr Glu Glu Arg Val Ser
180 185 190

Glu Gln Ile His Glu Lys Ile Phe Val Gly Arg Val Thr Asn Lys Gln
195 200 205

Ser Asp Ile Val Asn Ser Phe Ile Asn Gly Leu Leu Gln Lys Asp Arg
210 215 220

Asn Glu Leu Lys Asp Met Leu Ile Glu Phe Ala Lys Gln Glu
225 230 235

<210> 45

<211> 232

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS7F

<400> 45

Met Thr Arg Val Glu Leu Ile Thr Arg Glu Phe Phe Lys Lys Asn Glu
1 5 10 15

Ala Thr Ser Lys Tyr Phe Gln Lys Ile Glu Ser Arg Arg Gly Glu Leu
20 25 30

Phe Ile Lys Phe Phe Met Asp Lys Leu Leu Ala Leu Ile Leu Leu Leu
35 40 45

Leu Leu Ser Pro Val Ile Ile Ile Leu Ala Ile Trp Ile Lys Leu Asp
50 55 60

Ser Lys Gly Pro Ile Phe Tyr Arg Gln Glu Arg Val Thr Arg Tyr Gly
65 70 75 80

Arg Ile Phe Arg Ile Phe Lys Phe Arg Thr Met Ile Ser Asp Ala Asp
85 90 95

Lys Val Gly Ser Leu Val Thr Val Gly Gln Asp Asn Arg Ile Thr Lys
100 105 110

Val Gly His Ile Ile Arg Lys Tyr Arg Leu Asp Glu Val Pro Gln Leu
115 120 125

Phe Asn Val Leu Met Gly Asp Met Ser Phe Val Gly Val Arg Pro Glu
130 135 140

Val Gln Lys Tyr Val Asn Gln Tyr Thr Asp Glu Met Phe Ala Thr Leu
145 150 155 160

Leu Leu Pro Ala Gly Ile Thr Ser Pro Ala Ser Ile Ala Tyr Lys Asp
165 170 175

Glu Asp Ile Val Leu Glu Glu Tyr Cys Ser Gln Gly Tyr Ser Pro Asp
180 185 190

Glu Ala Tyr Val Gln Lys Val Leu Pro Glu Lys Met Lys Tyr Asn Leu
195 200 205

Glu Tyr Ile Arg Asn Phe Gly Ile Ile Ser Asp Phe Lys Val Met Ile
210 215 220

Asp Thr Val Ile Lys Val Ile Lys
225 230

<210> 46

<211> 404

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS7G

<400> 46

Met Thr Lys Arg Gln Asn Ile Pro Phe Ser Pro Pro Asp Ile Thr Gln
1 5 10 15

Ala Glu Ile Asp Glu Val Ile Asp Thr Leu Lys Ser Gly Trp Ile Thr
20 25 30

Thr Gly Pro Lys Thr Lys Glu Leu Glu Arg Arg Leu Ser Val Phe Thr
35 40 45

Gly Thr Asn Lys Thr Val Cys Leu Asn Ser Ala Thr Ala Gly Leu Glu
50 55 60

Leu Val Leu Arg Ile Leu Gly Val Gly Pro Gly Asp Glu Val Ile Val
65 70 75 80

Pro Ala Met Thr Tyr Thr Ala Ser Cys Ser Val Ile Thr His Val Gly
85 90 95

Ala Thr Pro Val Met Val Asp Ile Gln Lys Asn Ser Phe Glu Met Glu
100 105 110

Tyr Asp Ala Leu Glu Lys Ala Ile Thr Pro Lys Thr Lys Val Ile Ile
115 120 125

Pro Val Asp Leu Ala Gly Ile Pro Cys Asp Tyr Asp Lys Ile Tyr Thr
130 135 140

Ile Val Glu Asn Lys Arg Ser Leu Tyr Val Ala Ser Asp Asn Lys Trp
145 150 155 160

Gln Lys Leu Phe Gly Arg Val Ile Ile Leu Ser Asp Ser Ala His Ser
165 170 175

Leu Gly Ala Ser Tyr Lys Gly Lys Pro Ala Gly Ser Leu Ala Asp Phe
180 185 190

Thr Ser Phe Ser Phe His Ala Val Lys Asn Phe Thr Thr Ala Glu Gly
195 200 205

Gly Ser Val Thr Trp Arg Ser His Pro Asp Leu Asp Asp Glu Glu Met
210 215 220

Tyr Lys Glu Phe Gln Ile Tyr Ser Leu His Gly Gln Thr Lys Asp Ala
225 230 235 240

Leu Ala Lys Thr Gln Leu Gly Ser Trp Glu Tyr Asp Ile Val Ile Pro
245 250 255

Gly Tyr Lys Cys Asn Met Thr Asp Ile Met Ala Gly Ile Gly Leu Val
260 265 270

Gln Leu Glu Arg Tyr Pro Ser Leu Leu Asn Arg Arg Arg Glu Ile Ile
275 280 285

Glu Lys Tyr Asn Ala Gly Phe Glu Gly Thr Ser Ile Lys Pro Leu Val
290 295 300

His Leu Thr Glu Asp Lys Gln Ser Ser Met His Leu Tyr Ile Thr His
305 310 315 320

Leu Gln Gly Tyr Thr Leu Glu Gln Arg Asn Glu Val Ile Gln Lys Met
325 330 335

Ala Glu Ala Gly Ile Ala Cys Asn Val His Tyr Lys Pro Leu Pro Leu
340 345 350

Leu Thr Ala Tyr Lys Asn Leu Gly Phe Glu Met Lys Asp Phe Pro Asn
355 360 365

Ala Tyr Gln Tyr Phe Glu Asn Glu Val Thr Leu Pro Leu His Thr Asn
370 375 380

Leu Ser Asp Glu Asp Val Glu Tyr Val Ile Glu Met Phe Leu Lys Ile
385 390 395 400

Val Ser Arg Asp

<210> 47

<211> 210

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> CPS7H

<400> 47

Met Val Glu Arg Asp Met Val Glu Arg Asp Thr Leu Val Ser Ile Ile
1 5 10 15

Met Pro Ser Trp Asn Thr Ala Lys Tyr Ile Ser Glu Ser Ile Gln Ser
20 25 30

Val Leu Asp Gln Thr His Gln Asn Trp Glu Leu Ile Ile Val Asp Asp
35 40 45

Cys Ser Asn Asp Glu Thr Glu Lys Val Val Ser His Phe Lys Asp Ser
50 55 60

Arg Ile Lys Phe Phe Lys Asn Ser Asn Asn Leu Gly Ala Ala Leu Thr
65 70 75 80

Arg Asn Lys Ala Leu Arg Lys Ala Arg Gly Arg Trp Ile Ala Phe Leu
85 90 95

Asp Ser Asp Asp Leu Trp His Pro Ser Lys Leu Glu Lys Gln Leu Glu
100 105 110

Phe Met Lys Asn Asn Gly Tyr Ser Phe Thr Tyr His Asn Phe Glu Lys
115 120 125

Ile Asp Glu Ser Ser Gln Ser Leu Arg Val Leu Val Ser Gly Pro Ala
130 135 140

Ile Val Thr Arg Lys Met Met Tyr Asn Tyr Gly Tyr Pro Gly Cys Leu
145 150 155 160

Thr Phe Met Tyr Asp Ala Asp Lys Met Gly Leu Ile Gln Ile Lys Asp
165 170 175

Ile Lys Lys Asn Asn Asp Tyr Ala Ile Leu Leu Gln Leu Cys Lys Lys
180 185 190

Tyr Asp Cys Tyr Leu Leu Asn Glu Ser Leu Ala Ser Tyr Arg Ile Arg
195 200 205

Lys Lys
210

<210> 48

<211> 101

<212> DNA

<213> Streptococcus suis

<220>

<221> misc_feature

<222> (1)..(101)

<223> N may be any nucleotide

<220>

<221> misc_feature

<223> 100 base pair repeat between CPS2G and CPS2H

<400> 48

aagggcacct ctataaactc ccaaaattgc gaatttggag ttacgaaagc cttgttaaat 60

caancatttt aaattttaga aaattagttt ttagagctcc c 101

<210> 49

<211> 101

<212> DNA

<213> Streptococcus suis

<220>

<221> misc_feature

<222> (1)..(101)

<223> N may be any nucleotide

<220>

<221> misc_feature

<223> 100 base pair repeat within CPS2M

<400> 49

ggcgccacct ctataaattc ccaaaattgc gaatttcgag ttacgaaagc cttgttaaat 60

caancatctt aaattttaga aaattagttt ttagaggtcc c 101

<210> 50

<211> 101

<212> DNA

<213> Streptococcus suis

<220>

<221> misc_feature

<223> 100 base pair repeat between CPS2O and CPS2P

<400> 50

aagggcacct ctataaactc ccaaaattgc gaatttcgag ttacgaaagc cttgttaaat 60

caaacatttt aaattttaga aaattagttt ttagaggtcc c 101

<210> 51

<211> 120

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> N-terminal part of CPS2J

<400> 51

Met Ala Lys Val Ser Ile Ile Val Pro Ile Phe Asn Thr Glu Lys Tyr
1 5 10 15

Leu Arg Glu Cys Leu Asp Ser Ile Ile Ser Gln Ser Tyr Thr Asn Leu
20 25 30

Glu Ile Leu Leu Ile Asp Asp Gly Ser Ser Asp Ser Ser Thr Asp Ile
35 40 45

Cys Leu Glu Tyr Ala Glu Gln Asp Gly Arg Ile Lys Leu Phe Arg Leu
50 55 60

Pro Asn Gly Gly Val Ser Asn Ala Arg Asn Tyr Gly Ile Lys Asn Ser
65 70 75 80

Thr Ala Asn Tyr Ile Met Phe Val Asp Ser Asp Asp Ile Val Asp Gly
85 90 95

Asn Ile Val Glu Ser Leu Tyr Thr Cys Leu Lys Glu Asn Asp Ser Asp
100 105 110

Leu Ser Gly Gly Leu Leu Ala Thr
115 120

<210> 52

<211> 120

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> N-terminal part of CPS2K

<220>

<221> misc_feature

<222> (1)..(120)

<223> Xaa may be any amino acid

<400> 52

Met Ile Asn Ile Ser Ile Ile Val Pro Ile Tyr Asn Val Glu Gln Tyr
1 5 10 15

Leu Ser Lys Cys Ile Asn Ser Ile Val Asn Gln Thr Tyr Lys His Ile
20 25 30

Glu Leu Leu Val Asn Asp Gly Ser Ser Thr Asp Asn Ser Glu Glu Ile
35 40 45

Cys Leu Ala Tyr Ala Lys Lys Asp Ser Arg Ile Arg Tyr Phe Lys Lys
50 55 60

Glu Asn Gly Gly Leu Ser Asp Ala Arg Asn Tyr Gly Ile Ser Arg Ala
65 70 75 80

Lys Gly Asp Tyr Leu Ala Phe Ile Asp Ser Asp Asp Phe Ile His Ser
85 90 95

Glu Phe Ile Gln Arg Leu Xaa His Glu Ala Ile Glu Arg Glu Asn Ala
100 105 110

Leu Xaa Xaa Val Ala Val Ala Gly
115 120

<210> 53

<211> 419

<212> PRT

<213> Streptococcus suis

<220>

<221> misc_feature

<223> ORF2Y

<400> 53

Met Lys Lys Tyr Gln Val Ile Ile Gln Asp Ile Leu Thr Gly Ile Glu
1 5 10 15

Glu His Arg Phe Lys Arg Gly Glu Lys Leu Pro Ser Ile Arg Gln Leu
20 25 30

Arg Glu Gln Tyr His Cys Ser Lys Asp Thr Val Gln Lys Ala Met Leu
35 40 45

Glu Leu Lys Tyr Gln Asn Lys Ile Tyr Ala Val Glu Lys Ser Gly Tyr
50 55 60

Tyr Ile Leu Glu Asp Arg Asp Phe Gln Asp His Thr Cys Arg Ala Gln
65 70 75 80

Ser Tyr Arg Leu Ser Arg Ile Thr Tyr Glu Asp Phe Arg Ile Cys Leu
85 90 95

Lys Glu Ser Leu Ile Gly Arg Glu Asn Tyr Leu Phe Asn Tyr Tyr His
100 105 110

Gln Gln Glu Gly Leu Ala Glu Leu Ile Ser Ser Val Gln Ser Leu Leu
115 120 125

Met Asp Tyr His Val Tyr Thr Lys Lys Asp Gln Leu Val Ile Thr Ala
130 135 140

Gly Ser Gln Gln Ala Leu Tyr Ile Leu Thr Gln Met Glu Thr Leu Ala
145 150 155 160

Gly Lys Thr Glu Ile Leu Ile Glu Asn Pro Thr Tyr Ser Arg Met Ile
165 170 175

Glu Leu Ile Arg His Gln Gly Ile Pro Tyr Gln Thr Ile Glu Arg Asn
180 185 190

Leu Asp Gly Ile Asp Leu Glu Glu Leu Glu Ser Ile Phe Gln Thr Gly
195 200 205

Lys Ile Lys Phe Phe Tyr Thr Ile Pro Arg Leu His Asn Pro Leu Gly
210 215 220

Ser Thr Tyr Asp Ile Ala Thr Lys Thr Ala Ile Val Lys Leu Ala Lys
225 230 235 240

Gln Tyr Asp Val Tyr Ile Ile Glu Asp Asp Tyr Leu Ala Asp Phe Asp
245 250 255

Ser Ser His Ser Leu Pro Leu His Tyr Leu Asp Thr Asp Asn Arg Val
260 265 270

Ile Tyr Ile Lys Ser Phe Thr Pro Thr Leu Phe Pro Ala Leu Arg Ile
275 280 285

Gly Ala Ile Ser Leu Pro Asn Gln Leu Arg Asp Ile Phe Ile Lys His
290 295 300

Lys Ser Leu Ile Asp Tyr Asp Thr Asn Leu Ile Met Gln Lys Ala Leu
305 310 315 320

Ser Leu Tyr Ile Asp Asn Gly Met Phe Ala Arg Asn Thr Gln His Leu
325 330 335

His His Ile Tyr His Ala Gln Trp Asn Lys Ile Lys Asp Cys Leu Glu
340 345 350

Lys Tyr Ala Leu Asn Ile Pro Tyr Arg Ile Pro Lys Gly Ser Val Thr
355 360 365

Phe Gln Leu Ser Lys Gly Ile Leu Ser Pro Ser Ile Gln His Met Phe
370 375 380

Gly Lys Cys Tyr Tyr Phe Ser Gly Gln Lys Ala Asp Phe Leu Gln Ile
385 390 395 400

Phe Phe Glu Gln Asp Phe Ala Asp Lys Leu Glu Gln Phe Val Arg Tyr
405 410 415

Leu Asn Glu

REFERENCES

1. Arends, J. P., and H. C. Zanen. 1988. Meningitis caused by *Streptococcus suis* in humans. Rev. Infect. Dis. 10:131-37.

2. Arrecubieta, C., E. Garcia, and R. Lopez. 1995. Sequence and transcriptional analysis of a DNA region involved in the production of capsular polysaccharide in *Streptococcus pneumoniae* type 3. Gene 167: 1-7

3. Arrecubieta, C., R. Lopez, and E. Garcia. 1994. Molecular characterization of *cap3A,* a gene from the operon required for the synthesis of the capsule of *Streptococcus pneumoniae* type 3: sequencing of mutations responsible for the unencapsulated phenotype and localization of the capsular cluster on the pneumococcal chromosome. J. Bacteriol. 176: 6375-6383.

4. Clifton-Hadley, F.A. 1983. *Streptococcus suis* type 2 infections. Br. Vet. J. 139:1-5.

5. Charland, N., J. Harel, N., Kobisch, S. Lacasse, and M. Gottschalk. 1998. Streptococcus suis serotype 2 mutants deficient in capsular expression. Microbiol. 144:325-332.

6. Cross, A. S. 1990. The biological significance of bacterial encapsulation. Curr. Top. Microbiol. Immunol. 150: 87-95.

7. Elliott, S. D. and J. Y. Tai. 1978. The type specific polysaccharide of *Streptococcus suis.* J. Exp. Med. 148: 1699-1704.

8. Feder, I., M. M. Chengappa, B. Fenwick, M. Rider and J. Staats. 1994. Partial characterization of *Streptococcus suis* type 2 hemolysin. J. Clin. Microbiol. 32:1256-1260.

9. Gottschalk, M., R. Higgins, M. Jacques, M. Beaudoin, and J. Henrichsen. 1991. Characterization of six new capsular types (23 through 28) of *Streptococcus suis.* J. Clin. Microbiol. 29:2590-2594.

10. Gottschalk, M., S. Lacouture, and J. D. Dubreuil. 1995. Characterization of *Streptococcus suis* type 2 haemolysin. Microbiology 141:189-195.

11. Gottschalk, M., A. Lebrun, M. Jacques, and R. Higgins. 1990. Haemagglutination properties of *Streptococcus suis.* J. Clin. Microbiol. 28:2156-2158.

12. Guidolin, A., J. M. Morona, R. Morona, D. Hansman, and J. C. Paton. 1994. Nucleotide sequence analysis of genes essential for capsular polysaccharide biosynthesis in *Streptococcus pneumoniae* type 19F. 1994. Infect. Immun. 62: 5384-5396.

13. Guitierrez, C., and J. C. Devedjian. 1989. Plasmid facilitating *in vitro* construction of PhoA fusions in *Escherichia coli.* Nucl. Acid. Res. 17: 3999.

14. Higgins, R., M. Gottschalk, M. Boudreau, A. Lebrun, and J. Henrichsen. 1995. Description of six new capsular types (28 through 34) of *Streptococcus suis.* J. Vet. Diagn. Invest. 7: 405-406

15. Jacobs, A. A., P. L. W. Loeffen, A. J. G. van den Berg, and P. K. Storm. 1994. Identification, purification and characterization of a thiol-activated hemolysin (suilysin) of *Streptococcus suis.* Infect. Immun. 62: 1742-1748.

16. Jacques, M., M. Gottschalk, B. Foiry B. and R. Higgins. 1990. Ultrastructural study of surface components of *Streptococcus suis.* J. Bacteriol. 172:2833-2838.

17. Klein P., M. Kanehisa and C. DeLisi. 1985. The detection and classification of membrane spanning proteins. Biochim. Biophys. Acta. 851: 468-476.

18. Kolkman, M. A. B., D. A. Morrison, B. A. M. van der Zeijst, and P. J. M. Nuijten. 1996. The capsule polysaccharide synthesis locus of *Streptococcus pneumoniae* serotype 14: identification of the glycosyl transferase gene *cps14E.* J. Bacteriol. 178: 3736-3541.

19. Kolkman, M. A. B., W. Wakarchuk, P. J. M. Nuijten, and B. A. M. van der Zeijst. 1997. Capsular polysaccharide synthesis in *Streptococcus pneumoniae* serotype 14: molecular analysis of the complete *cps* locus and identification of genes encoding glycosyltransferases required for the biosynthesis of the tetrasaccharide subunit. Mol. Microbiol. 26: 197-208.

20. Kolkman, M. A. B., B. A. M. van der Zeijst and P. J. M. Nuijten. 1997. Functional analysis of glycosyltransferases encoded by the capsular polysaccharide biosynthesis locus of *Streptococcus pneumoniae* serotype 14. J. Biol. Chem. 272: 1950219508.

21. Konings, R. N. H., E. J. M. Verhoeven, and B. P H. Peeters. 1987. pKUN vectors for the separate production of both DNA strands of recombinant plasmids. Methods Enzymol. 153: 12-34.

22. Korolik, V., B. N. Fry, M. R. Alderton, B. A. M. van der zeijst, and P. J. Coloe. 1997. Expression of *Campylobacter hyoilei* lipo-oligosaccharide (LOS) antigens in *Escherichia coli.* Microbiol. 143: 3481-3489.

23. Leij, P. C. J., R. van Furth, and T. L. van Zwet. 1986. In vitro determination of phagocytosis and intracellular killing of polymorphonuclear and mononuclear phagocytes. In Handbook of Experimental Immunology, vol. 2. Cellular immunology, pp. 46.1-46.21. Edited by D. M. Weir, L. A. Herzenberg, C. Blackwell and L. A. Herzenberg. Blackwell scientific Publications, Oxford.

24. Lin, W. S., T. Cunneen, and C. Y. Lee. 1994. Sequence analysis and molecular characterization of genes required for the biosynthesis of type 1 capsular polysaccharide in *Staphylococcus aureus.* J. Bacteriol. 176: 7005-7016.

25. Liu, D., A. M. Haase, L. Lindqvist, A.A. Lindberg, and P. R. Reeves. 1993. Glycosyl transferases of O-antigen biosynthesis in *Salmonella enteritica:* Identification and characterization of transferase genes of group B, C2, and E1. J. Bacteriol. 175: 3408-3413.

26. Manoil, C., and J. Beckwith. 1985. A transposon probe for protein export signals. Proc. Natl. Acad. Sci. USA 82: 8129-8133.

27. Marsh, J. L., M. Erfle, and E. J. Wykes. 1984. The pIC plasmid and phage vectors with versatile cloning sites for recombinant selection by insertional inactivation. Gene 32:481-485.

28. Miller, J. 1972. Experiments in Molecular Genetics. Cold Spring Harbor, NY: Cold Spring Harbor Laboratory.

29. Morona, J. K., R. Morona, and J. C. Paton. 1997. Characterization of the locus encoding the *Streptococcus pneumoniae* type 19F capsular polysaccharide biosynthesis pathway. Mol. Microbiol. 23: 761-763.

30. Muñoz, R., M. Mollerach, R. López and E. Garcia. 1997. Molecular organization of the genes required for the synthesis of type 1 capsular polysaccharide of *Streptococcus pneumoniae;* formation of binary encapsulated pneumococci and identification of cryptic dTDP-rhamnose biosynthesis genes. Mol. Microbiol. 25: 79-92.

31. Pearce B. J., Y. B. Yin, and H. R. Masure. 1993. Genetic identification of exported proteins in *Streptococcus pneumoniae.* Mol. Microbiol. 9: 1037-1050.

32. Roberts, I. S. 1996. The biochemistry and genetics of capsular polysaccharide production in bacteria. Ann. Rev. Microbiol. 50: 285-315.

33. Rossbach, S., D. A. Kulpa, U. Rossbach, and F. J. de Bruin. 1994. Molecular and genetic characterization of the rhizopine catabolism (rnocABRC) genes of *Rhizobium meliloti* L5-30. Mol. Gen. Genet. 245: 11-24.

34. Rubens, C. E., L. M. Heggen, R. F. Haft, and R. M. Wessels. 1993. Identification of *cpsD*, a gene essential for type III capsule expression in group B streptococci. Mol. Microbiol. 8: 843-855.

35. Rubens, C. E., L. M. R. Wessels, L. M. Heggen, and D. L. Kasper. 1987. Transposon mutagenesis of type III group B Streptococcus correlation of capsule expression with virulence. Proc. Natl. Acad. Sci. USA 84:7208-7212.

36. Sambrook, J., E. F. Fritsch, and T. Maniatis. 1989. Molecular cloning. A laboratory manual. Second edition. Cold Spring Harbor Laboratory Press. Cold Spring Harbor. New York.

37. Smith, H. E., U. Vecht, H. J. Wisselink, N. Stockhofe-Zurwieden, Y. Biermann, and M. A. Smits. 1996. Mutants of *Streptococcus suis* types 1 and 2 impaired in expression of muramidase-released protein and extracellular protein induce disease in newborn germfree pigs. Infect Immun. 64: 4409-4412.

38. Smith, H. E., H. J. Wisselink, U. Vecht, A. L. J. Gielkens and M. A. Smits. 1995. High-efficiency transformation and gene inactivation in *Streptococcus suiss* type 2. Microbiol. 141: 181-188.

39. Sreenivasan, P. K., D. L. LeBlanc, L. N. Lee, and P. Fives-Taylor. 1991. Transformation of *Actinobacillus actinomycetemcomitans* by electroporation, utilizing constructed shuttle plasmids. Infect. Immun. 59: 4621-4627.

40. Stringele F., J.R. Neeser, and B. Mollet. 1996. Identification and characterization of the *eps* (exopolysaccharide) gene cluster from *Streptococcus thermophilus* Sfi6. J. Bacteriol. 178: 1680-1690.

41. Stockhofe-Zurwieden, N., U. Vecht, H. J. Wisselink, H. van Lieshout, and H. E. Smith. 1996. Comparative studies on the pathogenicity of different *Streptococcus suis* serotype 1 strains. In Proceedings of the 14th IPVS Congress. pp. 299.

42. van Kranenburg, R., J. D. Marugg, I. I. van Swam, N. J. Willem and W. M. de Vos. 1997. Molecular characterization of the plasinid-encoded *eps* gene cluster essential for exopolysaccharide biosynthesis in *Lactococcus lactis* Mol. Microbiol. 24: 387-397.

43. van Leengoed, L. A., E. M. Kamp, and J. M. A. Pol. 1989. Toxicity of *Haemophilus pleuropneumoniae* to porcine lung macrophages. Vet. Microbiol. 19: 337-349.

44. van Leengoed, L. A. M. G., U. Vecht, and E. R. M. Verheyen. 1987. *Streptococcus suis* type 2 infections in pigs in The Netherlands (part two). Vet Quart. 9, 111-117.

45. Vecht, U., J. P. Arends, E. J. van der Molen, and L. A. M. G. van Leengoed. 1989. Differences in virulence between two strains of *Streptococcus suis* type 2 after experimentally induced infection of newborn germfree pigs. Am. J. Vet. Res. 50:1037-1043.

46. Vecht, U., L. A. M. G. van Leengoed, and E. R. M. Verheyen. 1985. *Streptococcus suis* infections in pigs in The Netherlands (part one). Vet. Quart. 7:315-321.

47. Vecht, U., H. J. Wisselink, M. L. Jellema, and H. E. Smith. 1991. Identification of two proteins associated with virulence of *Streptococcus suis* type 2. Infect. Immun. 59:3156-3162.

48. Vecht, U., H. J. Wisselink, N. Stockhofe-Zurwieden, and H. E. Smith. 1996. Characterization of virulence of the *Streptococcus suis* serotype 2 reference strain Henrichsen S. 735 in newborn gnotobiotic pigs. Vet. Microbiol. 51:125-136.

49. Vecht, U., H. J. Wisselink, J. E. van Dijk, and H. E. Smith. 1992. Virulence of *Streptococcus suis* type 2 strains in newborn germfree pigs depends on phenotype. Infect. Immun. 60: 550-556.

50. Wagenaar, F., G. L. Kok, J. M. Broekhuijsen-Davies, and J. M. A. Pol. 1993. Rapid cold fixation of tissue samples by microwave irradiation for use in electron microscopy. Histochemical J. 25: 719-725.

51. Wessels, M. R. and M. S. Bronze. 1994. Critical role of the group A streptococcal capsule in pharyngeal colonization and infection in mice. Proc. Natl. Acad. Sci. USA 91: 12238-12242.

52. Wessels, M. R., A. E. Moses, J. B. Goldberg, and T. J. DiCesare. 1991. Hyaluronic acid capsule is a virulence factor for mucoid group A streptococci. Proc. Natl. Acad. Sci. USA. 88: 8317-8321.

53. Yamane, K., M. Kumamano, and K. Kurita. 1996. The 25°-36° region of the *Bacillus subtilis* chromosome: determination of the sequence of a 146 kb segment and identification of 113 genes. Microbiol. 142: 3047-3056.

54. Butler, J. C., R. F. Breiman, H. B. Lipman, J. Hofmann, and R. R. Facklam. 1995. Serotype distribution of *Streptococcus pneumoniae* infections among preschool children in the United States, 1978-1994: implications for development of a conjugate vaccine. J. Infect. Dis. 171: 885-889.

55. Charland, N., M. Jacques, S. Lacoutre and M. Gottschalk. 1997. Characterization and protective activity of a monoclonal antibody against a capsular epitope shared by *Streptococcus suis* serotypes 1, 2 and 1/2. Microbiol. 143: 3607-3614.

56. Gottschalk, M., R. Higgins, M. Jacques, K. R. Mittal, and J. Henrichsen. Description of 14 new capsular types of *Streptococcus suis.* J. Clin. Microbiol. 27:2633-2636.

57. Heath, P. J., B. W. Hunt, and J. P. Duff. 1996. *Streptococcus suis* serotype 14 as a cause of pig disease in the UK. Vet. Rec. 2:450-451.

58. Hommez, J., L. A. Devrieze, J. Henrichsen, and F. Castryck. 1986. Identification and characterization of *Streptococcus suis.* Vet. Microbiol. 16:349-355.

59. Killper-Balz, R., and K. H. Schleifer. 1987. Streptococcus suis sp. nov. nom. rev. Int. J. Syst. Bacteriol. 37:160-162.

60. Kolkman, M. A. B., B. A. M. van der Zeijst, and P. J. M. Nuijten. 1998. Diversity of capsular polysaccharide synthesis gene clusters in *Streptococcus pneumoniae*. Submitted for publication.

61. Lee, J. C., S. Xu, A. Albus, and P. J. Livolsi. 1994. Genetic analysis of type 5 capsular polysaccharide expression by *Staphylococcus aureus.* J. Bacteriol. 176:4883-4889.

62. Reek, F. H., M. A. Smits, E. M. Kamp, and H. E. Smith. 1995. Use of multiscreen plates for the preparation of bacterial DNA suitable for PCR. BioTechniques 19: 282-285.

63. Sau, S., N. Bhasin, E. R. Wann, J. C. Lee, T. J. Foster, and C. Y. Lee. 1997. The *Staphylococcus aureus* allelic genetic loci for serotype 5 and 8 capsule expression contain the type-specific genes flanked by common genes. Microbiol. 143: 2395-2405.

64. Sau, S., and C. Y. Lee. 1996. Cloning of type 8 capsule genes and analysis of gene clusters for the production of different capsular polysaccharides in *Staphylococcus aureus.* J. Bacteriol. 178: 2118-2126.

65. Sau, S., and C. Y. Lee. 1997. Molecular characterization and transcriptional analysis of type 8 capsule genes in *Staphylococcus aureus.* J. Bacteriol. 179:1614-1621.

66. Smith, H. E., M. Rijnsburger, N. Stockhofe-Zurwieden, H. J. Wisselink, U. Vecht, and M. A. Smits. 1997. Virulent strains of *Streptococcus suis* serotype 2 and highly virulent strains of *Streptococcus suis* serotype 1 can be recognized by a unique ribotype profile. J. Clin. Microbiol. 35:1049-1053.

67. Yamazaki, M., L. Thorne, M. Mikolajczak, R. W. Armentrout, and T. J. Pollock. 1996. Linkage of genes essential for synthesis of a polysaccharide capsule in *Sphingomonas* strain S88. J. Bacteriol. 178:2676-2687.

68. Zhang, L., A. Al-Hendy, P. Toivanen. and M. Skurnik. 1993. Genetic organization and sequence of the *rfb* gene cluster of *Yersinia enterolitica* serotype O:3: similarities to the dTDP-L-rhamnose biosynthesis pathway of *Salmonella* and to the bacterial polysaccharide transport systems. Mol. Microbiol. 9: 309-321.

69. Clifton-Hadley, F.A. (1983). *Streptococcus suis* type 2 infections. Br. Vet. J. 139, 1-5.

70. Vecht, U., van Leengoed, L. A. M. G. and Verheyen, E. R. M. (1985). *Streptococcus suis* infections in pigs in The Netherlands (part one). Vet. Quart. 7, 315-321.

71. Arends, J. P. and Zanen, H. C. (1988). Meningitis caused by *Streptococcus suis* in humans. Rev. Infect. Dis. 10, 131-137.

72. Hommez, J., Devrieze, L.A., Henrichsen, J. and Castryck, F.(1986). Identification and characterization of *Streptococcus suis*. Vet. Microbiol. 16, 349-355.

73. Killper-Balz, R. and Schleifer, K. H. (1987). *Streptococcus suis* sp. nov. nom.rev. Int. J. Syst. Bacteriol. 37, 160-162.

74. Gottschalk, M., Higgins, R. and Jacques, M. (1993). Production of capsular material by *Streptococcus suis* serotype 2 under different conditions. Can. J. Vet. Res. 57, 49-52.

75. Higgins, R. and Gottschalk, M. (1990). Un update on *Streptococcus suis* identification. J. Vet. Diagn. Invest. 2, 249-252.

76. Gottschalk, M., Higgins, R., Jacques, M., Beaudoin, M. and Henrichsen, J. (1991). Characterization of six new capsular types (23 through 28) of *Streptococcus suis*. J. Clin. Microbiol. 29, 2590-2594.

77. Gottschalk, M., Higgins, R., Jacques, M., Mittal, K. R. and Henrichsen, J. (1989) Description of 14 new capsular types of *Streptococcuss suis* J. Clin. Microbiol. 27, 2633-2636.

78. Higgins, R., Gottschalk, M., Boudreau, M., Lebrun, A. and Henrichsen, J. (1995). Description of six new capsular types (28 through 34) of *Streptococcus suis*. J. Vet. Diagn. Invest. 7, 405-406.

79. Aarestrup, F. M., Jorsal, S. E. and Jensen, N. E. (1998). Serological characterization and antimicrobial susceptibility of *Streptococcus suis* isolates from diagnostic samples in Denmark during 1995 and 1996. Vet. Microbiol. 15, 59-66.

80. MacLennan, M., Foster, G., Dick, K., Smith, W. J. and Nielsen, B. (1996). *Streptococcus suis* serotypes 7, 8 and 14 from diseased pigs in Scotland. Vet Rec. 139, 423-424.

81. Sihvonen, L., Kurl, D. N. and Henrichsen, J. (1988). *Streptococcus suis* isolates from pigs in Finland. Acta Vet. Scand. 29, 9-13.

82. Boetner, A. G., Binder, M. and Bille-Hansen, V. (1987). *Streptococcus suis* infections in Danish pigs and experimental infection with *Streptococcus suis* serotype 7. Acta Path. Microbiol. Immunol. Scand. Sect. B, 95, 233-239.

83. Smith, H. E., Veenbergen, V., van der Velde, J., Damman, M., Wisselink, H. J. and Smits, M. A. (1999). The cps genes of *Streptococcus suis* serotypes 1, 2 and 9: development of rapid serotype-specific PCR assays. J. Clin. Microbiol. submitted.84 Smith, H. E., Damman, M., van der Velde, J., Wagenaar, F., Wisselink, H. J., Stockhofe-Zurwieden, N. and Smits, M. A. (1999). Identification and characterization of the cps locus of *Streptococcus suis* serotype 2: the capsule protects against phagocytosis and is an important virulence factor. Infect. Immun. 67, 1750-1756.

85. Miller, J. (1972). Experiments in Molecular Genetics. Cold Spring Harbor Laboratory, Cold Spring Harbor, NY.

86. Sambrook, J., E. F. Fritsch, and T. Maniatis. (1989). Molecular cloning: a laboratory manual. Cold Spring Harbor Laboratory, Cold Spring Harbor, NY.

87. Allen, A. and Maskell, D. (1996). The identification, cloning and mutagenesis of a genetic locus required for lipopolysaccharide biosynthesis in *Bordetella pertussis*. Mol. Microbiol. 19, 37-52.

88. Wang, L. and Reeves, P. R. (1998). Organization of *Escherichia coli* O157 O antigen gene cluster and identification of its specific genes. Infect. Immun. 66, 3545-3551.

89. Wisselink, H. J., Reek, F. H., Vecht, U., Stockhofe-Zurwieden, N., Smits, M. A. and Smith, H. E. (1999). Detection of virulent strains of *Streptococcus suis* type 2 and highly, virulent strains of Streptococcus suis type 1 in tonsillar specimens of pigs by PCR. Vet. Microbiol. 67, 143-157.

90. Konings, R. N. H., Verhoeven, E. J. M. and Peeters, B. P. H. (1987). pKUN vectors for the separate production of both DNA strands of recombinant plasmids. Methods Enzymol. 153, 12-34.